

F:2202-2209/Region: nucleotide-binding motif A (P-loop)
F:2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 56.7%; Score 38; DB 2; Length 4568;
Best Local Similarity 41.7%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWXRNRKVR 12

Db 1852 CFQWQSLRYIQ 1863

RESULT 10

B60950

apolipoprotein B-100 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994

C:Accession: B60950

R:Law, A.; Scott, J.

J. Lipid Res. 31, 1109-1120, 1990

A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL

A:Reference number: A60950; MUID:90324804; PMID:2373961

A:Accession: B60950

A:Molecule type: mRNA

A:Residues: 1-274 <LAW>

A>Note: authors translated the codon ATA for residue 8 as Val

C:Superfamily: apolipoprotein B

C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 55.2%; Score 37; DB 2; Length 274;

Best Local Similarity 66.7%; Pred. No. 27;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WXRNRKVR 12

Db 39 WDRNRKFR 47

RESULT 11

C70655

probable monooxygenase - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: C70655

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, M.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: C70655

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-489 <COL>

A:Cross-references: GB:Z83864; GB:AL123456; MUID:g3261687; PIDN:CAB06212.1; PID:e301250;

A:Experimental source: strain H37Rv

C:Genetics:

A:Gene: RV3854c

Query Match 55.2%; Score 37; DB 2; Length 489;

Best Local Similarity 54.5%; Pred. No. 47;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWXRNRKVR 11

Db 253 CQWPRNRKRM 263

RESULT 12

T39801

hypothetical sh3-containing protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T39801

R:McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, July 1999

A:Reference number: 221880

A:Accession: T39801

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-501 <MCD>

A:Cross-references: EMBL:AL109731; PIDN:CAB52037.1; GSPDB:GN00067; SPDB:SPBC19C2.10

A:Experimental source: strain 972h-; cosmid c19C2

C:Genetics:

A:Gene: SPDB:SPBC19C2.10

A:Map position: 2

A:Introns: 196/3

Query Match 55.2%; Score 37; DB 2; Length 501;

Best Local Similarity 60.0%; Pred. No. 48;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWXRNRK 10

Db 50 CTRWRNRK 59

RESULT 13

C84325

hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: C84325

R:Ng, W.W.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.

Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: C84325

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-584 <STO>

A:Cross-references: GB:AE004437; MUID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138

C:Genetics:

Query Match 55.2%; Score 37; DB 2; Length 584;

Best Local Similarity 41.7%; Pred. No. 56;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWXRNRKVR 12

Db 445 CFTWRNRKVR 456

RESULT 14

C96582

F511.22 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: C96582

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: C96582

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;Status: preliminary
;Molecule type: DNA
;Residues: 1-124 <STO>
;Cross-references: GB:AE005173; NID:g4587555; PIDN:AAD25786.1; GSPDB:GN00141
;Genetics:
;Gene: F1511.22
;Map position: 1

Query Match      53.7%; Score 36; DB 2; Length 124;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

y 2 FQWXRNRKV 11
| | | | |
b 11 FRWRSRRKI 20

RESULT 15
D2346
;Protein: hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
;Species: Nostoc sp.
;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
;Accession: AD2346
;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
NA Res. 8, 205-213, 2001
;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
;Reference number: AB1807; MUID:21595285; PMID:11759840
;Accession: AD2346
;Status: preliminary
;Molecule type: DNA
;Residues: 1-298 <KUR>
;Cross-references: GB:BA000019; PIDN:BA076022.1; PID:g17133459; GSPDB:GN00179
;Experimental source: strain PCC 7120
;Genetics:
;Gene: alr4323

Query Match      53.7%; Score 36; DB 2; Length 298;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

y 2 FQWXRNRKV 10
| | | | |
b 163 FHWQRNRYK 171

earch completed: February 21, 2003, 08:02:44
ob time : 11.6047 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

PM protein - protein search, using sw model

Run on: February 21, 2003, 07:28:06 ; Search time 5.2093 Seconds
(without alignments)
95.544 Million cell updates/sec

Title: US-09-743-107B-88

Perfect score: 67

Sequence: 1 CFQXRMRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	65	97.0	711	1 TRFL_HUMAN	P02788 homo sapien
2	48	71.6	708	1 TRFL_CAMDR	Q9tum0 camelus dro
3	48	71.6	708	1 TRFL_CAPHI	Q29477 capra hircu
4	40	59.7	292	1 NLA_DROME	Q9xz18 drosophila
5	40	59.7	695	1 TRFL_HORSE	Q77811 equus cabal
6	39	58.2	707	1 TRFL_MOUSE	P08071 mus musculu
7	38	56.7	146	1 RPOB_LIBAF	P41187 liberibacte
8	38	56.7	783	1 YNR2_CAEEL	Q21988 caenorhabdi
9	38	56.7	4568	1 DYHB_CHLRE	Q39565 chlamydomon
10	36	53.7	365	1 1A34_HUMAN	P30453 homo sapien
11	36	53.7	369	1 SP11_MYXVL	P12393 myxoma viru
12	36	53.7	428	1 SYH_CHLMU	Q9pij9 chlamydia m
13	36	53.7	749	1 VP4_ROTGA	Q04916 rotavirus (
14	35	52.2	62	1 RL2E_THETN	Q8r9ul thermosae
15	35	52.2	966	1 VIA_EBWV	Q00020 broad bean
16	35	52.2	1135	1 PHYC_SORBI	P93528 sorghum bic
17	34	50.7	214	1 VIF_SIVS4	P12505 simian immu
18	34	50.7	422	1 PAPA_CHICK	Q90678 g platelet-
19	34	50.7	428	1 SYH_CHLTPN	Q84547 chlamydia t
20	34	50.7	430	1 SYH_CHLTPN	Q92701 chlamydia p
21	34	50.7	455	1 KYIL_CAEEL	Q19910 caenorhabdi
22	34	50.7	480	1 YOS1_CAEEL	Q09309 caenorhabdi
23	34	50.7	500	1 TLCE_RICPR	O05962 rickettsia
24	34	50.7	522	1 COR1_SCHPO	O13688 schistosacch
25	34	50.7	663	1 PD11_HUMAN	Q9ulc6 homo sapien
26	34	50.7	765	1 Y008_HUMAN	Q15398 homo sapien
27	34	50.7	989	1 T100_HUMAN	Q75448 homo sapien
28	34	50.7	1202	1 JAG2_RAT	P97607 rattus norv
29	34	50.7	1238	1 JAG2_HUMAN	Q9y219 homo sapien
30	34	50.7	1247	1 JAG2_MOUSE	Q9gye5 mus musculu
31	34	50.7	2151	1 RRPL_SEOUB	P27314 seoul virus
32	34	50.7	4568	1 DYHC_CAEEL	Q19020 caenorhabdi
33	33.5	50.0	727	1 KOGA_RAT	P51556 rattus norv

ALIGNMENTS

RESULT 1

```

TRFL_HUMAN STANDARD; PRT: 711 AA.
AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96K24;
AC Q96K25;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DB Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;
DB Lactoferrin B; Lactoferrin C].
GN LTF OR LF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90384839; PubMed=2402455;
RA Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RT Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Connely O.M.;
RT Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang Q., Jimenez-Flores R., Richardson T.;
RT "Molecular cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RT "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cheng H., Chen X., Huan L.;
RT "cDNA cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]

```

```

34 33.5 50.0 730 1 KOGA_MOUSE O88673 mus musculu
35 33 49.3 62 1 RL28_STAAM Q99up4 staphylococ
36 33 49.3 144 1 REV_OMYVS P16903 ovine lenti
37 33 49.3 172 1 Y708_METJA Q58118 methanococc
38 33 49.3 211 1 PDOI_ECOLI P32174 escherichia
39 33 49.3 224 1 GTXA_ARATH P46421 arabidopsis
40 33 49.3 238 1 CCDA_BACHD Q9kd18 bacillus ha
41 33 49.3 246 1 Y495_SYNY3 Q55185 synecocyst
42 33 49.3 275 1 VAL6_VACCV P16710 vaccinia vi
43 33 49.3 378 1 VAL6_VACCV P20993 vaccinia vi
44 33 49.3 573 1 UREL_LACFE P28929 lactobacill
45 33 49.3 648 1 Z202_HUMAN O95125 homo sapien

```

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary Gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ouden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RA Legrand D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RA Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RA Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin.";
RL FEBS Lett. 142:1107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Choj L., la Bastide M., Kaplan N., Graco T., Touchman J., Mazny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Fang M., Porcel B.M., U.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desliva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe N., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253-->methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;

Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
"Structure of recombinant human lactoferrin expressed in Aspergillus
awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=1009508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational changes.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Baeti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier P., Schorderet D.F.,
RA El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejtmancik J.P., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
RN [21]
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- ACTIVITY: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
CC EMBL; X53961; CAA37914.1; -
CC EMBL; U07643; AAB60324.1; -
CC EMBL; M93150; AAB36159.1; -
CC EMBL; M83202; AAA59511.1; -
CC EMBL; M83205; AAA58656.1; -
CC EMBL; M18642; AAA86665.1; -
CC EMBL; AF332168; AAG48753.1; -
CC EMBL; BC015822; AAH15822.1; -
CC EMBL; BC015823; AAH15823.1; -
CC EMBL; M73700; AAA59479.1; -
CC EMBL; X52941; CAA37116.1; -
CC EMBL; U95626; AAB57795.1; -
CC PIR; S11228; TFHUL
CC PDB; 1LCF; 31-AUG-94.
CC PDB; 1LCT; 31-OCT-93.
CC PDB; 1LFG; 31-JUL-94.
CC PDB; 1LFH; 31-OCT-93.
CC PDB; 1LFI; 31-OCT-93.
CC PDB; 1LGB; 31-AUG-94.
CC PDB; 1LGC; 31-AUG-94.
CC PDB; 1BKA; 08-NOV-96.
CC PDB; 1DSN; 08-MAR-96.
CC PDB; 1HSE; 12-MAR-97.
CC PDB; 1VFD; 21-APR-97.

[illegible]


```
C or send an email to license@sib-sib.ch).
C -----
R EMBL; AF147700; AAD33987.1; -.
R EMBL; AE003712; AAF55285.1; -.
R FlyBase; FBgn0026629; nla.
Q SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

Query Match 59.7%; Score 40; DB 1; Length 292;
Best Local Similarity 54.5%; Pred. No. 2.6;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Y 2 FQWXRNMKVR 12
||| |.:.|
b 150 FQWLSFRRLR 160

RESULT 5
D TRFL HORSE STANDARD; PRT; 695 AA.
C 07811;
T 15-JUL-1999 (Rel. 38, Created)
T 15-JUL-1999 (Rel. 38, Last sequence update)
T 15-JUN-2002 (Rel. 41, Last annotation update)
E Lactotransferrin precursor (Lactoferrin) (Fragment).
N LTF.
S Equus caballus (Horse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
X NCBI_TaxID=9796;
N [1]
N SEQUENCE FROM N.A.
P Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
A "cDNA sequence of mare lactoferrin.";
T Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
L [2]
P X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
C TISSUE=Milk;
X MEDLINE=99296631; PubMed=10366507;
U Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
T "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
resolution.";
U J. Mol. Biol. 289:303-317(1999).
X -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
X -!- SUBUNIT: MONOMER.
X -!- SUBCELLULAR LOCATION: Secreted.
X -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
X -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
X -----
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X -----
R EMBL; AJ010930; CAA09407.1; -.
R PDB; 1B1X; 02-DEC-98.
R PDB; 1B7U; 02-FEB-99.
R PDB; 1B7Z; 02-FEB-99.
R InterPro; IPR001156; Transferrin.
R Pfam; PF00405; transferrin; 2.
R PRINTS; PR00422; TRANSFERRIN.
R SMART; SM00094; TR_FER; 2.
R PROSITE; PS00205; TRANSFERRIN_1; 2.
R PROSITE; PS00206; TRANSFERRIN_2; 2.
R PROSITE; PS00207; TRANSFERRIN_3; 1.
R Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal; 3d-structure.
W Signal 1 1
T NON_TER 1 1
T SIGNAL <1 6
```

```
FT CHAIN 7 695 LACTOTRANSFERRIN.
FT REPEAT 7 350 1.
FT REPEAT 351 695 2.
FT DISULFID 15 51
FT DISULFID 25 42
FT DISULFID 121 204
FT DISULFID 163 179
FT DISULFID 166 189
FT DISULFID 176 187
FT DISULFID 237 251
FT DISULFID 354 386
FT DISULFID 364 377
FT DISULFID 411 690
FT DISULFID 431 653
FT DISULFID 463 538
FT DISULFID 487 681
FT DISULFID 497 511
FT DISULFID 508 521
FT DISULFID 579 593
FT DISULFID 631 636
FT METAL 66 66 IRON 1 (BY SIMILARITY).
FT METAL 98 98 IRON 1 (BY SIMILARITY).
FT METAL 198 198 IRON 1 (BY SIMILARITY).
FT METAL 259 259 IRON 1 (BY SIMILARITY).
FT METAL 401 401 IRON 2 (BY SIMILARITY).
FT METAL 439 439 IRON 2 (BY SIMILARITY).
FT METAL 532 532 IRON 2 (BY SIMILARITY).
FT METAL 601 601 IRON 2 (BY SIMILARITY).
FT BINDING 127 127 ANION (BY SIMILARITY).
FT BINDING 469 469 ANION (BY SIMILARITY).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 482 482 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 59.7%; Score 40; DB 1; Length 695;
Best Local Similarity 58.3%; Pred. No. 6.1;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWXRNMKVR 12
||| |.:.|
DB 25 CAKEQNRNMKVR 36

RESULT 6
TRFL MOUSE STANDARD; PRT; 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=8728033; PubMed=3611056;
RA Pentecost B.T., Teng C.T.;
RT "Lactotransferrin is the major estrogen inducible protein of mouse
uterine secretions.";
RL J. Biol. Chem. 262:10134-10139 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Moriishi K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
```

Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

SEQUENCE OF 1-14 FROM N.A.
 MEDLINE=92042099; PubMed=1939212;
 Liu Y., Teng C.T.;
 J. Biol. Chem. 266:21880-21885(1991).
 FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
 SUBUNIT: MONOMER.
 DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 EMBL: J03298; AAA40525.1; -
 EMBL: D88510; BAA13633.1; -
 EMBL: BC006904; AAH06904.1; -
 EMBL: M74778; AAA39427.1; -
 PIR: A28438; A28438.
 HSP: P02788; 1CB6.
 MGD: MGI:98837; Lef.
 InterPro: IPR001156; Transferrin.
 Pfam: PF00405; transferrin; 2.
 PRINTS: P00422; TRANSFERRIN.
 SMART: SM00094; TR FER; 2.
 PROSITE: PS00205; TRANSFERRIN_1; 1.
 PROSITE: PS00206; TRANSFERRIN_2; 2.
 PROSITE: PS00207; TRANSFERRIN_3; 2.
 Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal.
 CHAIN 1 19 BY SIMILARITY.
 REPEAT 20 707 LACTOTRANSFERRIN.
 REPEAT 358 707 1.
 DISULFID 27 63 BY SIMILARITY.
 DISULFID 37 54 BY SIMILARITY.
 DISULFID 133 216 BY SIMILARITY.
 DISULFID 175 191 BY SIMILARITY.
 DISULFID 188 199 BY SIMILARITY.
 DISULFID 249 263 BY SIMILARITY.
 DISULFID 366 398 BY SIMILARITY.
 DISULFID 375 389 BY SIMILARITY.
 DISULFID 423 702 BY SIMILARITY.
 DISULFID 443 685 BY SIMILARITY.
 DISULFID 475 550 BY SIMILARITY.
 DISULFID 499 693 BY SIMILARITY.
 DISULFID 509 523 BY SIMILARITY.
 DISULFID 520 533 BY SIMILARITY.
 DISULFID 591 605 BY SIMILARITY.
 DISULFID 643 648 BY SIMILARITY.
 METAL 78 78 IRON 1 (BY SIMILARITY).
 METAL 110 110 IRON 1 (BY SIMILARITY).
 METAL 210 210 IRON 1 (BY SIMILARITY).
 METAL 271 271 IRON 1 (BY SIMILARITY).
 METAL 413 413 IRON 2 (BY SIMILARITY).
 METAL 451 451 IRON 2 (BY SIMILARITY).
 METAL 544 544 IRON 2 (BY SIMILARITY).
 METAL 613 613 IRON 2 (BY SIMILARITY).
 BINDING 139 139 ANION (POTENTIAL).
 BINDING 481 481 ANION (POTENTIAL).
 CARBOHYD 118 118 N-LINKED (GLCNAC...) (POTENTIAL).
 CARBOHYD 494 494 N-LINKED (GLCNAC...) (POTENTIAL).
 CONFLICT 1 2 MR -> IOG (IN REF. 1).
 CONFLICT 25 25 R -> Q (IN REF. 2).

FT CONFLICT 82 82 M -> L (IN REF. 2).
 FT CONFLICT 359 359 S -> T (IN REF. 2).
 FT CONFLICT 382 382 A -> D (IN REF. 1).
 FT CONFLICT 449 449 E -> G (IN REF. 2).
 FT CONFLICT 629 629 L -> V (IN REF. 1).
 SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;
 Query Match 58.2%; Score 39; DB 1; Length 707;
 Best Local Similarity 54.5%; Pred. No. 9.6;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CFQWXRNRKV 11
 DB 37 CLRQWNRKV 47
 RESULT 7
 ID RPOB LIBAF STANDARD; PRT; 146 AA.
 AC P41187;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
 DE RPOB.
 OS Liberibacter africanus (Liberibacter africanus).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Candidatus Liberibacter.
 OX NCBI_TaxID=34020;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nelspruit;
 RA Planet P., Jagoueix S., Bove J.M., Garnier M.;
 RT "Detection and characterization of the African Citrus Greening
 RT Liberibacter by amplification, cloning and sequencing of the rplKAJL-
 RT rpoBC operon";
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RC FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA) (N).
 CC SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
 CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
 CC BETA' CHAIN.
 CC SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
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 CC or send an email to license@isb-sib.ch)
 CC EMBL: U09675; AAA19557.1; -
 CC InterPro: IPR001572; RNA pol B.
 DR Pfam: PF00562; RNA pol B; 1.
 DR PROSITE: PS01166; RNA POL BETA; PARTIAL.
 KW Transferase; Transcription; DNA-directed RNA polymerase.
 FT NON_TER 146 146
 SQ SEQUENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
 Query Match 56.7%; Score 38; DB 1; Length 146;
 Best Local Similarity 60.0%; Pred. No. 3;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CFQWXRNRKV 10
 DB 10 CVQWNRGARK 19

RESULT 8

YR2_CABEL
ID YNR2_CABEL STANDARD; PRT; 783 AA.
AC Q21988;
JT 15-DEC-1998 (Rel. 37, Created)
JT 15-JUN-2002 (Rel. 41, Last sequence update)
JT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein R13G10.2 in chromosome III.
R13G10.2.
XN Caenorhabditis elegans.
XC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
XC Rhabditidae; Peloderinae; Caenorhabditis.
XX NCBI_TaxID=6239;
XN [1]
XN SEQUENCE FROM N.A.
XN STRAIN=Bristol N2;
XA Gardner A.E.;
XN Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
[2]
XN REVISIONS.
XA Durbin R.;
XN Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
XC -1- COFACTOR: FAD (POTENTIAL).
XC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
XC This SWISS-PROT entry is copyright. It is produced through a collaboration
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XC
XN EMBL; Z35602; CAA84671.2;
XN Wormpep; R13G10.2; CE25088.
XN InterPro; IPR002937; Amino oxidase.
XN Pfam; PF01593; Amino oxidase; 1.
XW Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
XN NP BIND 311 366 FAD (ADP PART) (POTENTIAL).
XN SEQUENCE 783 AA; 88799 MW; 8D087E96464DC908 CRC64;
Query Match 56.7%; Score 38; DB 1; Length 783;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Y 1 CFQWXRNMKVR 12
b 540 CIDWGRDRKVK 551
Query Match 56.7%; Score 38; DB 1; Length 783;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

RESULT 9

YHB_CHLRE
D_DYHB_CHLRE STANDARD; PRT; 4568 AA.
C Q3956;
T 01-NOV-1997 (Rel. 35, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
T 30-MAY-2000 (Rel. 39, Last annotation update)
E Dynein beta chain, flagellar outer arm.
N ODA4 OR ODA-4 OR SUP1.
S Chlamydomonas reinhardtii.
C Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
C Chlamydomonadaceae; Chlamydomonas.
X NCBI_TaxID=3055;
XN [1]
XN SEQUENCE FROM N.A.
XN STRAIN=21gr;
XN MEDLINE=94274778; PubMed=8006077;
XA Mitchell D.R.; Brown K.S.;
T "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
chain genes."
L J. Cell Sci. 107:635-644 (1994).
C -1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
C FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.

CC DYNEIN HAS ATPASE ACTIVITY.
CC -1- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
CC GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
CC -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
CC
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CC
CC EMBL; U02963; AAA19956.1;
DR InterPro; IPR004273; Dynein heavy.
DR Pfam; PF03028; Dynein heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
KW Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP BIND 1919 1926 ATP (POTENTIAL).
FT NP BIND 2202 2209 ATP (POTENTIAL).
FT NP BIND 2530 2537 ATP (POTENTIAL).
FT NP BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 56.7%; Score 38; DB 1; Length 4568;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWXRNMKVR 12
Db 1852 CFQWQSLRYIQ 1863
Query Match 56.7%; Score 38; DB 1; Length 4568;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 10

1A34_HUMAN
ID 1A34_HUMAN STANDARD; PRT; 365 AA.
AC P30453; P30454;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, AW-34(A-10) alpha chain
DE precursor.
GN HLA-A OR HLAA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*3401/A*3402).
RX MEDLINE=93056508; PubMed=1431115;
RA Madrigal J.A.; Belich M.P.; Hildebrand W.H.; Benjamin R.J.;
RA Little A.-M.; Zemmour J.; Ennis P.D.; Ward F.E.; Petzl-Erler M.L.;
RA Martell R.W.; du Toit E.D.; Farham P.;
RT "Distinctive HLA-A,B antigens of black populations formed by
interallelic conversion."
RL J. Immunol. 149:3411-3415 (1992).
RN [2]
RP SEQUENCE FROM N.A. (A*3401/A*3402).
RX MEDLINE=93235211; PubMed=8475492;
RA Madrigal J.A.; Hildebrand W.H.; Belich M.P.; Benjamin R.J.;
RA Little A.-M.; Zemmour J.; Ennis P.D.; Ward F.E.; Petzl-Erler M.L.;
RA du Toit E.D.; Farham P.;
RT "Structural diversity in the HLA-A10 family of alleles: correlations

```

RT with serology."
RL Tissue Antigens 41:72-80(1993).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -1- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401
CC (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
CC A*3401.
CC -----
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CC -----
DR EMBL; X61704; CAA43873.1; -
DR EMBL; X61705; CAA43874.1; -
DR PIR; S16767; S16767.
DR PIR; S16771; S16771.
DR HSSP; O19673; IHSB.
DR MIM; 142800; -
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; ig_1.
DR Pfam; PF00129; MHC_I; 1.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365
FT -----
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT AW-34(A*10) ALPHA CHAIN.
FT -----
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 130
FT DISULFID 125. 188
FT DISULFID 227 283
FT VARIANT 3 3
FT VARIANT 90 90
FT VARIANT 121 121
FT VARIANT 129 129
FT VARIANT 138 138
FT VARIANT 180 180
FT VARIANT 312 312
FT SEQUENCE 365 AA; 41055 MW; 063BF63E5E6E01F6 CRC64;
SQ
Query Match 53.7%; Score 36; DB 1; Length 365;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 WXRNRKRV 12
Db 84 WDRNRKRV 92
RESULT 11
SP11_MXXVL
ID SP11_MXXVL STANDARD; PRT; 369 AA.

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AC P12393;
DT 01-OCT-1999 (Rel. 12, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
GN SERINE PROTEINASE INHIBITOR 1 (Serp1) (Serp-1).
GN SERP1 OR M008.1L.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OC NCBI_TaxID=31530;
OX [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=91049428; PubMed=2173255;
RA Upton C., Macen J.L., Wishart D.S., McFadden G.;
RA "Myxoma virus and malignant rabbit fibroma virus encode a serpin-like
RT protein important for virus virulence.";
RL Virology 179:618-631(1990).
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=87064296; PubMed=3023828;
RA Upton C., McFadden G.;
RA "DNA sequence homology between the terminal inverted repeats of Shope
RT fibroma virus and an endogenous cellular plasmid species.";
RL Mol. Cell. Biol. 6:265-276(1986).
RN [3]
RX SEQUENCE FROM N.A.
RX MEDLINE=87030884; PubMed=3021526;
RA Upton C., Carrell R.W., McFadden G.;
RA "A novel member of the serpin superfamily is encoded on a circular
RT plasmid-like DNA species isolated from rabbit cells.";
RL FEBS Lett. 207:115-120(1986).
RN [4]
RX SEQUENCE FROM N.A.
RX MEDLINE=20032073; PubMed=10562494;
RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
RA Macaulay C., Willer D., Evans D., McFadden G.;
RA "The complete DNA sequence of Myxoma virus.";
RL Virology 264:298-318(1999).
CC -1- FUNCTION: IMPORTANT IN VIRULENCE.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY. POXVIRUSES SUBFAMILY.
CC -1- CAUTION: WAS ORIGINALLY (REF.2 AND REF.3) THOUGHT TO ORIGINATE
CC FROM A PLASMID RABBIT DNA. THE ORIGINAL SAMPLE WAS CONTAMINATED
CC AND THE GENE IS DERIVED FROM MYXOMA VIRUS.
CC -----
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CC -----
DR EMBL; M35233; AAA46629.1; -
DR EMBL; M12333; AAA81567.1; -
DR EMBL; AF170726; AAF15055.1; -
DR EMBL; AF170726; AAF14896.1; -
DR PIR; A24470; A24470.
DR PIR; B36418; B36418.
DR HSSP; P05121; IB3K.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor; Virulence.
FT ACT_SITE 319 320 REACTIVE BOND (BY SIMILARITY).
FT CONFLICT 1 16 MKYLVLCVLSACR -> MFWVVRV (IN REF. 2
FT AND 3).
FT SEQUENCE 369 AA; 41556 MW; 8DB31CE131C218A0 CRC64;
SQ
Query Match 53.7%; Score 36; DB 1; Length 369;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Y 4 WXRNRK 10
b 235 WXRNRK 241

RESULT 12
YH CHLMU
D SYH CHLMU STANDARD; PRT; 428 AA.
C QPJJ9;
T 16-OCT-2001 (Rel. 40, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
E Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
E (Hiss).
N HISS OR TC0830.
N HISS OR TC0830.
S Chlamydia muridarum.
C Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
X NCBI_TaxID=83560;
[1]
N N
P SEQUENCE FROM N.A.
C STRAIN=MoPn / Ni99;
X MEDLINE=20150255; PubMed=10684935;
A Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
A White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
A Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
A Winn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
A Eisen J., Fraser C.M.;
T "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
T pneumoniae AR39.";
L Nucleic Acids Res. 28:1397-1406(2000).
C -1- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
C diposphate + L-histidyl-tRNA(His).
C -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
C -1- SUBCELLULAR LOCATION: Cytoplasmic.
C -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-tRNA SYNTHETASE FAMILY.
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C or send an email to license@isb-sib.ch).
C
C EMBL; AE002349; AAP39630.1; -
C HSP; O32422; IQE0.
C TIGR; TC0830; -
C InterPro; IPR002106; AATRNA_ligaseII.
C InterPro; IPR004154; HGTP_anticonodon.
C InterPro; IPR004516; Hiss.
C Pfam; PF00587; tRNA-synt_2b; 1.
C Pfam; PF03129; HGTP_anticonodon; 1.
C TIGRPFAMS; TIGR00442; hiss; 1.
R POSITE; PS50862; AA_TRNA_LIGASE_II; 1.
W Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
W Complete proteome.
Q SEQUENCE 428 AA; 48939 MW; 9CF859ED0E689DDF CRC64;

Query Match 53.7%; Score 36; DB 1; Length 428;
Best Local Similarity 44.4%; Pred. No. 21;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Y 1 CFQWXRNR 9
b 348 CFSWAKHLR 356

RESULT 13
P4 ROTGA
D VP4 ROTGA STANDARD; PRT; 749 AA.
C Q04916;
T 01-JUN-1994 (Rel. 29, Created)

01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
S4.
OS Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=12705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9333240; PubMed=8396274;
RA Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.;
RT "Identification and baculovirus expression of the VP4 protein of the
RT human group B rotavirus ADRV.";
RL J. Virol. 67:2730-2738(1993).
CC -1- SUBCELLULAR LOCATION: Outer capsid.
CC -1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
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CC
C EMBL; M91434; AAA47338.1; -
C InterPro; IPR000416; Cap_VP4.
C Pfam; PF00426; VP4; 1.
X Coat protein; Glycoprotein.
FT CARBOHYD 29 29 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 568 568 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 681 681 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 749 AA; 84362 MW; D1223527DEAE0F21 CRC64;

Query Match 53.7%; Score 36; DB 1; Length 749;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CFQWXRNRKVR 12
Db 195 CFTWDMKNCANVR 206

RESULT 14
RL28 THETN
ID RL28 THETN STANDARD; PRT; 62 AA.
AC Q8R9U1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L28.
GN RPB OR TTE1495.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ME4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.

```

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CC -----
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CC -----
DR EMBL; AE013107; AM24713.1; -
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;

Query Match 52.2%; Score 35; DB 1; Length 62;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWXRNRKVR 12
Db :|:|:|:|
27 RWKPNIRKVR 36

RESULT 15
VIA_BMV VIA_BMV STANDARD; PRT; 966 AA.
AC Q00020;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1A protein [includes: Helicase; Methyltransferase].
OS Broad bean mottle virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Bromovirus.
OX NCBI_TaxID=12301;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bawden;
RX MEDLINE=92074218; PubMed=1962437;
RA Dzanott A.M., Bujarski J.J.;
RT "The nucleotide sequence and genome organization of the RNA-1 segment
RT in two bromoviruses: broad bean mottle virus and cowpea chlorotic
RT mottle virus."
RL Virology 185:553-562(1991).
CC -!- FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CC CONTAINS AN HELICASE DOMAIN AND A METHYLTRANSFERASE DOMAIN. THE
CC METHYLTRANSFERASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA
CC CAPPING.
CC -!- SIMILARITY: TO 1A PROTEIN FROM CCMV, CMV, PSV AND TAV.
CC -----
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CC -----
DR EMBL; M65138; AAA42740.1; -
DR PIR; A41699; PIBVBE.
DR InterPro; IPR002588; V_methyltransf.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF01443; Viral_helicase1.
DR Pfam; PF01660; Vmethyltransf.1.
KW Helicase; ATP-binding; Transferase; Methyltransferase.
FT NF_BIND 690 697 ATP (POTENTIAL):CRC64;
SQ SEQUENCE 966 AA; 109621 MW; DF528681D7231C8D CRC64;

Query Match 52.2%; Score 35; DB 1; Length 966;
Best Local Similarity 46.7%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 1 CFQ----WXRNRKVR 11
||:|:|:|
```

Db 347 CFKKNKDWTEENRSV 361

Search completed: February 21, 2003, 07:51:36
Job time : 6.2093 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
(without alignments)
114.078 Million cell updates/sec

Title: US-09-743-107b-88

Perfect score: 67

Sequence: 1 CFQWXRNRKV 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	89.6	711	4 Q8TCD2	Q8tcd2 homo sapien
2	56	83.6	38	4 Q9UCY5	Q9ucy5 homo sapien
3	45	67.2	33	6 Q9TR80	Q9tr80 ovine aries
4	41	61.2	511	16 Q8Z462	Q8z462 salmonella
5	40	59.7	148	10 Q9XHP1	Q9xhp1 sesamum ind
6	40	59.7	273	2 Q31090	Q31090 rhizobium l
7	39	58.2	275	5 Q93780	Q93780 caenorhabdi
8	39	58.2	341	11 Q8R2A4	Q8r2a4 mus musculu
9	39	58.2	415	5 Q9U4M9	Q9u4m9 leishmania
10	39	58.2	866	10 Q9FH19	Q9fhi9 arabidopsis
11	38	56.7	108	9 Q8SC55	Q8sc55 stx2 conver
12	38	56.7	372	10 Q81553	Q81553 hemerocalli
13	38	56.7	531	10 Q9S1C0	Q9s1c0 arabidopsis
14	37	55.2	91	15 Q77855	Q77855 human immun
15	37	55.2	91	15 Q77856	Q77856 human immun
16	37	55.2	179	11 Q9CZQ7	Q9czq7 mus musculu

17	37	55.2	233	11	Q9D4X5	Q9d4x5 mus musculu
18	37	55.2	274	4	Q96M21	Q96m21 homo sapien
19	37	55.2	279	16	Q8XSE2	Q8xse2 rallostonia s
20	37	55.2	329	12	Q9QB73	Q9qb73 yaba monkey
21	37	55.2	368	11	Q9DAJ3	Q9daj3 mus musculu
22	37	55.2	368	11	Q9D9X0	Q9d9x0 mus musculu
23	37	55.2	368	11	Q9JIT1	Q9jit1 mus musculu
24	37	55.2	377	12	Q9IMQ5	Q9imq5 lumpy skin
25	37	55.2	381	12	Q9DHK5	Q9dhk5 yaba-like d
26	37	55.2	489	16	P96223	P96223 mycobacteri
27	37	55.2	501	3	Q9UUD0	Q9uud0 schizosacch
28	37	55.2	570	10	Q8A487	Q8a487 zea mays (m
29	37	55.2	584	17	Q9HPA3	Q9hpa3 halobacteri
30	37	55.2	2348	5	Q9V346	Q9v346 drosophila
31	36	53.7	105	10	Q9AFD5	Q9afd5 oryza sativ
32	36	53.7	109	15	Q9YQC1	Q9yqc1 human immun
33	36	53.7	109	15	Q9YQC0	Q9yqc0 human immun
34	36	53.7	109	15	Q9YQB9	Q9yqb9 human immun
35	36	53.7	109	15	Q9YQB8	Q9yqb8 human immun
36	36	53.7	109	15	Q9YJ17	Q9yj17 human immun
37	36	53.7	109	15	Q9YJ12	Q9yj12 human immun
38	36	53.7	119	15	Q8Q454	Q8q454 human immun
39	36	53.7	124	10	Q9SYH0	Q9syh0 arabidopsis
40	36	53.7	298	16	Q8YF77	Q8yfp77 anabaena sp
41	36	53.7	306	4	Q8TAX2	Q8tax2 homo sapien
42	36	53.7	466	4	Q9NUS2	Q9nus2 homo sapien
43	36	53.7	514	5	Q9V118	Q9v118 drosophila
44	36	53.7	514	10	Q9SP27	Q9sp27 callistephu
45	36	53.7	543	5	Q9XZ30	Q9xz30 drosophila

ALIGNMENTS

RESULT 1

Q8TCD2 ID Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RL Strausberg R.;
DR EMBL; BC022347; AAH22347.1; -
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 89.6%; Score 60; DB 4; Length 711;
Best Local Similarity 90.9%; Pred. No. 0.003; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 1 CFQWXRNRKV 11
DB 39 CFQWXRNRKV 49

RESULT 2

Q9UCY5 ID Q9UCY5 PRELIMINARY; PRT; 38 AA.
AC Q9UCY5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96061613; PubMed=8551695;
 RA Sato I.;
 RT "Characterization of the 84-kDa protein with ABH activity in human
 RT seminal plasma";
 RL Jpn. J. Legal Med. 49:281-293 (1995).
 DR HSP; P02788; 18KA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EDDEB CRC64;

Query Match 83.6%; Score 56; DB 4; Length 38;
 Best Local Similarity 90.9%; Pred. No. 0.0085;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 FQWXRNRKVR 12
 DB 21 FQWQRNRKVR 31

RESULT 3
 Q9TR80
 ID Q9TR80 PRELIMINARY; PRT; 33 AA.
 AC Q9TR80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Lactoferrin (fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]_TaxID=9940;
 RP SEQUENCE
 RX MEDLINE=95127729; PubMed=7827104;
 RA Qian Z.Y., Jolles P., Migliore-Samur D., Fiat A.M.;
 RL Blochim. Biophys. Acta 1243:125-32 (1995).
 DR HSP; O77698; 1CE2.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 67.2%; Score 45; DB 6; Length 33;
 Best Local Similarity 54.5%; Pred. No. 0.098;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWXRNRKV 11
 DB 19 CYQWQKVRKL 29

RESULT 4
 Q8Z462
 ID Q8Z462 PRELIMINARY; PRT; 511 AA.
 AC Q8Z462;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein STY3070.
 GN STY3070.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=601;
 RN [1]_TaxID=601;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 Krogan A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
 Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RT Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18";
 RL Nature 413:848-852 (2001).
 DR EMBL; AL627276; CAD06049.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 511 AA; 58126 MW; E2DD124510D178B CRC64;

Query Match 61.2%; Score 41; DB 16; Length 511;
 Best Local Similarity 58.3%; Pred. No. 9.9;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CFQWXRNRKVR 12
 DB 350 CFQWQNRKVR 361

RESULT 5
 Q9XHP1
 ID Q9XHP1 PRELIMINARY; PRT; 148 AA.
 AC Q9XHP1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE 2S albumin.
 OS Sesamum indicum (Oriental sesame) (gingelly).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
 OX NCBI_TaxID=4182;
 RN [1]_TaxID=4182;
 RP SEQUENCE FROM N.A.
 RC STRAIN=TAINAN 1;
 RX MEDLINE=20074970; PubMed=10606554;
 RA Tai S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
 RL "Molecular cloning of 11S globulin and 2S albumin, the two major seed
 RL storage proteins in sesame";
 RL J. Agric. Food Chem. 47:4932-4938 (1999).
 DR EMBL; AF091841; AAD42943.1; -;
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR000817; Napin.
 DR InterPro; IPR001768; Try/amyL_inhbr.
 DR Pfam; PF00234; trypan_alpha_amy1; 1.
 DR PRINTS; PR00496; NAFIN.
 DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 59.7%; Score 40; DB 10; Length 148;
 Best Local Similarity 66.7%; Pred. No. 4.3;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWXRNRMR 9
 DB 54 CFQWQNRMR 62

RESULT 6
 Q31090
 ID Q31090 PRELIMINARY; PRT; 273 AA.
 AC Q31090;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Hypothetical 31.0 kDa protein.
 OS Rhizobium leguminosarum (biovar viciae).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.

X NCBI_TaxID=387;
 N [1]
 P SEQUENCE FROM N.A.
 C STRAIN=VF39;
 A Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N.;
 L Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 N [2]
 P SEQUENCE FROM N.A.
 C STRAIN=VF39;
 X MEDLINE=99113394; PubMed=9914965;
 A Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G.,
 Ksenzenko V.N.;
 T "Structural and functional organization of the exopolysaccharide
 biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39";
 L Mol. Biol. (Mosk) 32:797-804 (1998).
 R EMBL; AF028810; AAB8891.1; -;
 W Hypothetical protein.
 Q SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 273;
 Best Local Similarity 60.0%; Pred. No. 8.1;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Y 3 QWXRNMKVR 12
 : : : : :
 b 245 RWLRNLRKLR 254

RESULT 7
 93780
 D Q93780 PRELIMINARY; PRT; 275 AA.
 C Q93780;
 T 01-FEB-1997 (TrEMBLrel. 02, Created)
 T 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 E F53H4.4 protein.
 N N
 S Caenorhabditis elegans.
 C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 C Rhabditidae; Peloderinae; Caenorhabditis.
 X NCBI_TaxID=6239;
 N [1]
 P SEQUENCE FROM N.A.
 A Dobson R.;
 L Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 N [2]
 P SEQUENCE FROM N.A.
 X MEDLINE=99069613; PubMed=9851916;
 A none;
 T "Genome sequence of the nematode C.elegans: A platform for
 investigating biology";
 L Science 282:2012-2018 (1998).
 R EMBL; Z81089; CAB03137.1; -;
 Q SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 58.2%; Score 39; DB 5; Length 275;
 Best Local Similarity 63.6%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Y 2 FQWXRNMKVR 12
 : : : : :
 b 262 FQWXRNMKVR 272

RESULT 8
 8R2A4
 D Q8R2A4 PRELIMINARY; PRT; 341 AA.
 C Q8R2A4;
 T 01-JUN-2002 (TrEMBLrel. 21, Created)
 T 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 T 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 E Vomeroneasal receptor V1RE6.
 N V1RE6.
 P SEQUENCE FROM N.A.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129X1/SVJ;
 RX MEDLINE=21676859; PubMed=11802169;
 RA Rodriguez I., Del Punta K., Rothman A., Ishii T., Mombaerts P.;
 RT "Multiple new and isolated families within the mouse superfamily of
 Vir vomeronasal receptors";
 RL Nat. Neurosci. 5:134-140 (2002).
 DR EMBL; AY065506; AAL47911.1; -;
 XW Receptor.
 SQ SEQUENCE 341 AA; 39632 MW; B3D8259F7AD11130 CRC64;

Query Match 58.2%; Score 39; DB 11; Length 341;
 Best Local Similarity 55.6%; Pred. No. 16;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWXRNM 9
 : : : : :
 Db 331 CFQWXRNM 339

RESULT 9
 Q9U4M9
 ID Q9U4M9 PRELIMINARY; PRT; 415 AA.
 AC Q9U4M9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE 7138.2.
 GN 7138.2.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PRIEDLIN;
 RA Ravel C., Dubessay P., Blaineau C., Lignon M.-F., Bastien P.,
 Dedet J.-P., Pages M.;
 RT "Leishmania major chromosome 5 complete sequence";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF163772; AAF14642.1; -;
 DR InterPro: IPR003409; MORN.
 DR Pfam: PF02493; MORN; 4.
 SQ SEQUENCE 415 AA; 46701 MW; 3E3AD710BF23691E CRC64;

Query Match 58.2%; Score 39; DB 5; Length 415;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWXRNM 9
 : : : : :
 Db 272 CGEWFNR 280

RESULT 10
 Q9FH19
 ID Q9FH19 PRELIMINARY; PRT; 866 AA.
 AC Q9FH19;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Genomic DNA, chromosome 5, p1 clone:MFC19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.

```

RC STRAIN=COLUMBIA;
RX MEDLINE=99397451; PubMed=10470850;
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
RT Sequence features of the regions of 1,011,550 bp covered by seventeen
RT P1 and TAC clones.";
RL DNA Res. 6:183-195(1999).
DR EMBL; AB018113; BAB09175.1; -.
SQ SEQUENCE 866 AA; 100187 MW; 164FAB9B4976D27D CRC64;

Query Match 58.2%; Score 39; DB 10; Length 866;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWXRNRKVR 12
Db 389 CFNWLKFKRLR 400
|||:|
|:|

RESULT 11
Q8SC55 PRELIMINARY; PRT; 108 AA.
AC Q8SC55;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 12.3 kDa protein.
OS Stx2 converting bacteriophage I.
OC Viruses.
OX NCBI_TaxID=180816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STX2 PHAGE-I;
RA Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hanabata T.,
RA Yamasaki S., Takeda Y.;
RT "Genomic sequence of Shiga toxin 2-converting phage isolated from
RT Escherichia coli O157:H7 Okayama strain and comparison with other
RT Shiga toxin 2-converting phages.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF004402; BAB87947.1; -.
KW Hypothetical protein.
SQ SEQUENCE 108 AA; 12279 MW; 2FF2E76690C78BA7 CRC64;

Query Match 56.7%; Score 38; DB 9; Length 108;
Best Local Similarity 60.0%; Pred. No. 7.5;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWXRNRK 10
Db 31 CFQWISNRK 40
|||:|
|:|

RESULT 12
O81653 PRELIMINARY; PRT; 372 AA.
AC O81653;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Senescence-associated protein 3 (fragment).
GN SA3.
OS Hemerocallis hybrid cultivar.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
OC Hemerocallidaceae; Hemerocallis.
OX NCBI_TaxID=80862;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. STELLA D'ORO; TISSUE=SENESCING PETALS;
RX MEDLINE=99339248; PubMed=10412903;
RA Panavas T., Pikula A., Reid P.D., Rubinstein B., Walker E.L.;
RT "Identification of senescence-associated genes from daylily petals.";
```

```

RL Plant Mol. Biol. 40:237-248(1999).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF082028; AAC34853.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PRO0385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON TER 1
SQ SEQUENCE 372 AA; 41909 MW; 55FB3EAF96959595E CRC64;

Query Match 56.7%; Score 38; DB 10; Length 372;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWXRN 7
Db 328 CFWDNRN 334
|||:|
|:|

RESULT 13
Q9SICO PRELIMINARY; PRT; 531 AA.
AC Q9SICO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE En/Spm-like transposon protein.
GN AT2G05650.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buehl C.R., Ketchum K.A., Lee J.-J., Renning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nietman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007170; AAD25641.1; -.
DR InterPro; IPR004264; Transposase_23.
DR Pfam; PF03017; Transposase_23; 1.
SQ SEQUENCE 531 AA; 60512 MW; 57B3AC60C976A4B9 CRC64;

Query Match 56.7%; Score 38; DB 10; Length 531;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWXRNRK 10
Db 501 QWFRNRK 508
|||:|
|:|

RESULT 14
Q77855 PRELIMINARY; PRT; 91 AA.
AC Q77855;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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GenCore version 5.1.3
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DM protein - protein search, using sw model

Run on: February 21, 2003, 07:37:21 ; Search time 28.093 Seconds
(without alignments)
56.918 Million cell updates/sec

Title: US-09-743-107B-89

Perfect score: 66

Sequence: 1 CFQWQRMRKVR 12

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	98.5	12	21 AAY78074	Human lactoferrin
2	64	97.0	12	21 AAY78038	Human lactoferrin
3	64	97.0	12	21 AAY78046	Human lactoferrin
4	64	97.0	12	21 AAY78047	Human lactoferrin
5	64	97.0	12	21 AAY78086	Human lactoferrin
6	64	97.0	12	21 AAY78089	Human lactoferrin
7	64	97.0	12	21 AAY78090	Human lactoferrin
8	64	97.0	13	21 AAY78037	Human lactoferrin
9	64	97.0	13	21 AAY78048	Human lactoferrin
10	64	97.0	13	21 AAY78049	Human lactoferrin

11	64	97.0	14	21 AAY78036	Human lactoferrin
12	64	97.0	14	21 AAY78050	Human lactoferrin
13	64	97.0	14	21 AAY78051	Human lactoferrin
14	64	97.0	15	17 AAY8554	Peptide for anti-u
15	64	97.0	15	21 AAY78035	Human lactoferrin
16	64	97.0	15	21 AAY78062	Human lactoferrin
17	64	97.0	15	21 AAY78063	Human lactoferrin
18	64	97.0	16	21 AAY78031	Human lactoferrin
19	64	97.0	16	21 AAY78064	Human lactoferrin
20	64	97.0	16	21 AAY78065	Human lactoferrin
21	64	97.0	17	21 AAY78034	Human lactoferrin
22	64	97.0	17	21 AAY78066	Human lactoferrin
23	64	97.0	17	21 AAY78067	Human lactoferrin
24	64	97.0	18	15 AAY8352	Human lactoferrin
25	64	97.0	18	17 AAY13397	Advanced glycosyla
26	64	97.0	18	21 AAY78033	Human lactoferrin
27	64	97.0	19	21 AAY68867	Amino acid sequenc
28	64	97.0	19	21 AAY78032	Human lactoferrin
29	64	97.0	20	13 AAY21810	Anti microbial pep
30	64	97.0	20	14 AAY44841	Lactoferrin-relate
31	64	97.0	20	15 AAY48530	Lactoferrin derive
32	64	97.0	20	15 AAY48531	Lactoferrin derive
33	64	97.0	20	15 AAY57461	Lactoferrin derive
34	64	97.0	20	15 AAY57462	Lactoferrin derive
35	64	97.0	20	16 AAY84698	Bovine lactoferrin
36	64	97.0	20	16 AAY84699	Bovine lactoferrin
37	64	97.0	20	16 AAY80263	Anti-parasitic lac
38	64	97.0	20	16 AAY80264	Anti-parasitic lac
39	64	97.0	20	17 AAY98553	Peptide for anti-u
40	64	97.0	20	17 AAY91852	Lactoferrin-derive
41	64	97.0	20	17 AAY03045	Lactoferrin-derive
42	64	97.0	20	17 AAY90607	Lactoferrin-derive
43	64	97.0	20	17 AAY87621	Lactoferrin-derive
44	64	97.0	20	17 AAY87622	Lactoferrin-derive
45	64	97.0	20	18 AAY26150	Lactoferrin deriva

ALIGNMENTS

RESULT 1

AAY78074

ID AAY78074 standard; Peptide; 12 AA.

XX AAY78074;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:74.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

PD 13-JAN-2000.

XX 06-JUL-1999; 99WO-SB01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections, -
PT inflammations and tumors and for use in infant formula food
XX
XX Claim 22; Page 35; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX Sequence 12 AA;
SQ
Query Match 98.5%; Score 65; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 5.3e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRXMKVR 12
DB 1 CFQWQRXMKVR 12

RESULT 2
AAY78038
ID AAY78038 standard; Peptide; 12 AA.
XX
AC AAY78038;
XX
DT 25-APR-2000 (first entry)
DE Human lactoferrin derived peptide SEQ ID NO:38.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2000001730-A1.
PN
XX 13-JAN-2000.
PD
XX
XX 06-JUL-1999; 99WO-SE01230.
PF
XX
XX 06-JUL-1998; 98SE-0002441.
PR
XX 17-JUL-1998; 98SE-0002562.
PR
XX 29-DEC-1998; 98SE-0004614.
PR
XX
XX (ASCI-) A+ SCI INVEST AB.
PA
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI
XX WPI; 2000-147388/13.
DR
XX
XX New peptides used for treatment and prevention of infections, -
PT inflammations and tumors and for use in infant formula food
XX
XX Claim 12; Page 70; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX Sequence 12 AA;
SQ
Query Match 97.0%; Score 64; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRXMKVR 12
DB 1 CFQWQRXMKVR 12

RESULT 3
AAY78046
ID AAY78046 standard; Peptide; 12 AA.
XX
AC AAY78046;
XX
DT 25-APR-2000 (first entry)
DE Human lactoferrin derived peptide SEQ ID NO:46.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2000001730-A1.
PN
XX 13-JAN-2000.
PD
XX
XX 06-JUL-1999; 99WO-SE01230.
PF
XX
XX 06-JUL-1998; 98SE-0002441.
PR
XX 17-JUL-1998; 98SE-0002562.
PR
XX 29-DEC-1998; 98SE-0004614.
PR
XX
XX (ASCI-) A+ SCI INVEST AB.
PA
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI
XX WPI; 2000-147388/13.
DR
XX
XX New peptides used for treatment and prevention of infections, -
PT inflammations and tumors and for use in infant formula food
XX
XX Claim 15; Page 35; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

XX fungicidal and bactericidal and may also be used as preservatives.
 XX Even though native human lactoferrin have been shown to have desired
 XX anti-inflammatory anti-infectious and anti-tumoural properties they
 XX cannot be used clinically on a broad basis because of high production
 XX costs. Therefore, provision of peptides based on lactoferrin would
 XX enable them to be used for the same purposes as lactoferrin at lower
 XX cost.

XX Sequence 12 AA;

Query Match 97.0%; Score 64; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQWQXMRKVR 12
 | | | | |
 Db 1 CFQWQXMRKVR 12

RESULT 4
 AAY78047
 ID AAY78047 standard; Peptide; 12 AA.

XX AAY78047;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:47.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX urinary tract infection; colitis; Candida infection; fungicidal;
 XX bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -

XX Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through
 XX binding to specific lactoferrin receptors and are then transported
 XX through the circulation. A medicinal product of the peptide or fragment
 XX can be used for treating and/or prevention of infections (such as
 XX urinary tract infections, colitis, and Candida infection on a mucosal
 XX membrane), inflammations and/or tumours. The peptides can also be used
 XX in food stuffs such as infant formula food. The peptides are also
 XX fungicidal and bactericidal and may also be used as preservatives.
 XX Even though native human lactoferrin have been shown to have desired
 XX anti-inflammatory anti-infectious and anti-tumoural properties they
 XX cannot be used clinically on a broad basis because of high production
 XX costs. Therefore, provision of peptides based on lactoferrin would
 XX enable them to be used for the same purposes as lactoferrin at lower
 XX cost.

XX Sequence 12 AA;

Query Match 97.0%; Score 64; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQXMRKVR 12
 | | | | |
 Db 1 CFQWQXMRKVR 12

RESULT 5
 AAY78086
 ID AAY78086 standard; Peptide; 12 AA.

XX AAY78086;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:86.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX urinary tract infection; colitis; Candida infection; fungicidal;
 XX bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -

XX Claim 22; Page 36; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through
 XX binding to specific lactoferrin receptors and are then transported
 XX through the circulation. A medicinal product of the peptide or fragment
 XX can be used for treating and/or prevention of infections (such as
 XX urinary tract infections, colitis, and Candida infection on a mucosal
 XX membrane), inflammations and/or tumours. The peptides can also be used
 XX in food stuffs such as infant formula food. The peptides are also
 XX fungicidal and bactericidal and may also be used as preservatives.
 XX Even though native human lactoferrin have been shown to have desired
 XX anti-inflammatory anti-infectious and anti-tumoural properties they
 XX cannot be used clinically on a broad basis because of high production
 XX costs. Therefore, provision of peptides based on lactoferrin would
 XX enable them to be used for the same purposes as lactoferrin at lower
 XX cost.

XX Sequence 12 AA;

Query Match 97.0%; Score 64; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
 Db 1 CFQWQXMRKVR 12

RESULT 6

AAV78089
 ID AAY78089 standard; Peptide; 12 AA.

XX AAY78089;

XX 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:89.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 22; Page 37; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;

Query Match 97.0%; Score 64; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.9e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12

Db 1 CFQWQXMRKVR 12

RESULT 7

AAV78090

ID AAY78090 standard; Peptide; 12 AA.

XX AAY78090;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:90.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 22; Page 37; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;

Query Match 97.0%; Score 64; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.9e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12

Db 1 CFQWQXMRKVR 12

RESULT 8

AAV78037

ID AAY78037 standard; Peptide; 13 AA.

XX AAY78037;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 DS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 VI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 70; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through
 XX binding to specific lactoferrin receptors and are then transported
 XX through the circulation. A medicinal product of the peptide or fragment
 XX can be used for treating and/or prevention of infections (such as
 XX urinary tract infections, colitis, and Candida infection on a mucosal
 XX membrane), inflammations and/or tumors. The peptides can also be used
 XX in food stuffs such as infant formula food. The peptides are also
 XX fungicidal and bactericidal and may also be used as preservatives.
 XX Even though native human lactoferrin have been shown to have desired
 XX anti-inflammatory anti-infectious and anti-tumoural properties they
 XX cannot be used clinically on a broad basis because of high production
 XX costs. Therefore, provision of peptides based on lactoferrin would
 XX enable them to be used for the same purposes as lactoferrin at lower
 XX cost.
 XX Sequence 13 AA;
 XX
 XX Query Match 97.0%; Score 64; DB 21; Length 13;
 XX Best Local Similarity 91.7%; Pred. No. 8.6e-05;
 XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1 CFQWQXMRKVR 12
 XX |||||
 XX 2 CFQWQXMRKVR 13
 XX
 XX RESULT 9
 XX AAY78048
 XX ID AAY78048 standard; Peptide; 13 AA.
 XX
 XX AAY78048;
 XX
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:48.
 XX
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX urinary tract infection; colitis; Candida infection; fungicidal;
 XX bactericidal; preservative.
 XX Homo sapiens.

OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 VI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 74; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through
 XX binding to specific lactoferrin receptors and are then transported
 XX through the circulation. A medicinal product of the peptide or fragment
 XX can be used for treating and/or prevention of infections (such as
 XX urinary tract infections, colitis, and Candida infection on a mucosal
 XX membrane), inflammations and/or tumors. The peptides can also be used
 XX in food stuffs such as infant formula food. The peptides are also
 XX fungicidal and bactericidal and may also be used as preservatives.
 XX Even though native human lactoferrin have been shown to have desired
 XX anti-inflammatory anti-infectious and anti-tumoural properties they
 XX cannot be used clinically on a broad basis because of high production
 XX costs. Therefore, provision of peptides based on lactoferrin would
 XX enable them to be used for the same purposes as lactoferrin at lower
 XX cost.
 XX Sequence 13 AA;
 XX
 XX Query Match 97.0%; Score 64; DB 21; Length 13;
 XX Best Local Similarity 91.7%; Pred. No. 8.6e-05;
 XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1 CFQWQXMRKVR 12
 XX |||||
 XX 2 CFQWQXMRKVR 13
 XX
 XX RESULT 10
 XX AAY78049
 XX ID AAY78049 standard; Peptide; 13 AA.
 XX
 XX AAY78049;
 XX
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:49.
 XX
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX urinary tract infection; colitis; Candida infection; fungicidal;
 XX bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.

XX		
PR	06-JUL-1998;	98SE-0002441.
PR	17-JUL-1998;	98SE-0002562.
PR	29-DEC-1998;	98SE-0004614.
XX		
PA	(ASCII-) A+ SCI INVEST AB.	

XX	06-JUL-1998;	98SE-0003441.
XX	PR	Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX	PI	WPI; 2000-147388/13.
XX	DR	(ASCI-) A+ SCI INVEST AB.
XX	PA	Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX	PT	New peptides used for treatment and prevention of infection
XX	PT	inflammations and tumors and for use in infant formula
XX	PS	Claim 18: Page 74: 102pp. English.

AA78001 to AA79100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and *Candida* infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.

PI	Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX	
DR	WPI; 2000-147388/13.
XX	
PT	New peptides used for treatment and prevention of infections, -
PT	inflammations and tumors and for use in infant formula food
XX	
PS	Claim 12; Page 69; 102pp; English.
PS	
XX	AA778001 to AA778100 represent peptides having sequences based on human
CC	lactoferrin. The peptides are taken up in the intestine through
CC	binding to specific lactoferrin receptors and are then transported
CC	through the circulation. A medicinal product of the peptide or fragment
CC	can be used for treating and/or prevention of infections (such as
CC	urinary tract infections, colitis, and Candida infection on a mucosal
CC	membrane), inflammations and/or tumours. The peptides can also be used
CC	in food stuffs such as infant formula food. The peptides are also
CC	fungicidal and bactericidal and may also be used as preservatives.
CC	Even though native human lactoferrin have been shown to have desired
CC	anti-inflammatory anti-infectious and anti-tumoural properties they
CC	cannot be used clinically on a broad basis because of high production
CC	costs. Therefore, provision of peptides based on lactoferrin would
CC	enable them to be used for the same purposes as lactoferrin at lower
CC	cost.
CC	

```

XX      Sequence    14 AA;
Query Match          97.0%; Score 64; DB 21; Length 14;
Best Local Similarity 91.7%; Pred. No. 9.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CFQWQRXMRKVR 12
        |||||
Db       3 CFQWQRNWRKVR 14
        |||||

RESULT 12
AAAY78050
ID   AAY78050 standard; Peptide; 14 AA.
XX
AC   AAY78050;
XX
DT   25-APR-2000 (first entry)

```

XX	Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
PI	
XX	
XX	
XX	WPI; 2000-147388/13.
XX	
XX	New peptides used for treatment and prevention of infections,
PT	inflammations and tumors and for use in infant formula food
PT	
XX	
XX	

2S Claim 15; Page 75; 102pp; English.

3C AAY78001 to AAY78100 represent peptides having sequences based on human
 3C lactoferrin. The peptides are taken up in the intestine through
 3C binding to specific lactoferrin receptors and are then transported
 3C through the circulation. A medicinal product of the peptide or fragment
 3C can be used for treating and/or prevention of infections (such as
 3C urinary tract infections, colitis, and Candida infection on a mucosal
 3C membrane), inflammations and/or tumours. The peptides can also be used
 3C in food stuffs such as infant formula food. The peptides are also
 3C fungicidal and bactericidal and may also be used as preservatives.
 3C Even though native human lactoferrin have been shown to have desired
 3C anti-inflammatory anti-infectious and anti-tumoural properties they
 3C cannot be used clinically on a broad basis because of high production
 3C costs. Therefore, provision of peptides based on lactoferrin would
 3C enable them to be used for the same purposes as lactoferrin at lower
 3C cost.

3Q Sequence 14 AA;

Query Match 97.0%; Score 64; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 9.2e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3Y 1 CFQWQRMKVR 12
 ||||| |||||
 3b 3 CFQWQRMKVR 14

RESULT 13
 AAY78051
 ID AAY78051 standard; Peptide; 14 AA.

3C AAY78051;

3D 25-APR-2000 (first entry)

3E Human lactoferrin derived peptide SEQ ID NO:51.

3F Human; lactoferrin; modification; infection; inflammation; tumour;
 3G food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 3H urinary tract infection; colitis; Candida infection; fungicidal;
 3I bactericidal; preservative.

3J Homo sapiens.
 3K Synthetic.

3L WO200001730-A1.

3M 13-JAN-2000.

3N 06-JUL-1999; 99WO-SB01230.2

3O 06-JUL-1998; 98SE-0002441.
 3P 17-JUL-1998; 98SE-0002562.
 3Q 29-DEC-1998; 98SE-0004614.
 3R (ASCI-) A+ SCI INVEST AB.

3S Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 3T WPI; 2000-147388/13.

3U New peptides used for treatment and prevention of infections,
 3V inflammations and tumors and for use in infant formula food -
 3W Claim 18; Page 75; 102pp; English.

3X AAY78001 to AAY78100 represent peptides having sequences based on human
 3Y lactoferrin. The peptides are taken up in the intestine through
 3Z binding to specific lactoferrin receptors and are then transported
 3A through the circulation. A medicinal product of the peptide or fragment
 3B can be used for treating and/or prevention of infections (such as

3C urinary tract infections, colitis, and Candida infection on a mucosal
 3D membrane), inflammations and/or tumours. The peptides can also be used
 3E in food stuffs such as infant formula food. The peptides are also
 3F fungicidal and bactericidal and may also be used as preservatives.
 3G Even though native human lactoferrin have been shown to have desired
 3H anti-inflammatory anti-infectious and anti-tumoural properties they
 3I cannot be used clinically on a broad basis because of high production
 3J costs. Therefore, provision of peptides based on lactoferrin would
 3K enable them to be used for the same purposes as lactoferrin at lower
 3L cost.

3M Sequence 14 AA;

Query Match 97.0%; Score 64; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 9.2e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3N 1 CFQWQRMKVR 12
 ||||| |||||
 3O 3 CFQWQRMKVR 14

RESULT 14
 AAR98554
 ID AAR98554 standard; Peptide; 15 AA.

3P AC AAR98554;

3Q 12-NOV-1996 (first entry)

3R Peptide for anti-ulcer agent.

3S anti-ulcer agent; low toxicity; stable; heat-resistant.

3T Synthetic.

3U JP08143468-A.

3V 04-JUN-1996.

3W 17-NOV-1994; 94JP-0283869.

3X 17-NOV-1994; 94JP-0283869.

3Y (MORG) MORINAGA MILK IND CO LTD.

3Z WPI; 1996-318857/32.

3A Anti-ulcer agent contg. peptide - has low toxicity, is
 3B heat-resistant and water-soluble

3C Claim 1; Page 11; 11pp; Japanese.

3D AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
 3E in toxicity, is heat-resistant and stable in aqueous soln.. It can be
 3F administered orally and be produced in large amounts.

3G Sequence 15 AA;

Query Match 97.0%; Score 64; DB 17; Length 15;
 Best Local Similarity 91.7%; Pred. No. 9.8e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3H 1 CFQWQRMKVR 12
 ||||| |||||
 3I 2 CFQWQRMKVR 13

RESULT 15
 AAY78035
 ID AAY78035 standard; Peptide; 15 AA.

3K AC AAY78035;

```
XX
DT
XX
DE
XX
XX 25-APR-2000 (first entry)
DE Human lactoferrin derived peptide SEQ ID NO:35.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 12; Page 69; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX Sequence 15 AA;
XX
Query Match 97.0%; Score 64; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 9.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQRMKVR 12
DB 4 CFQWQRMKVR 15
| | | | |
| | | | |
```

Search completed: February 21, 2003, 07:56:43
Job time : 28.093 secs

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XM protein - protein search, using sw model

run on: February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds
(without alignments)
39.537 Million cell updates/sec

Title: US-09-743-107B-89
Perfect score: 66
Sequence: 1 CFQQRXMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/6C COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	64	97.0	18	1 US-08-204-487-3	Sequence 3, Appli
2	64	97.0	18	2 US-08-485-948-8	Sequence 8, Appli
3	64	97.0	18	2 US-08-628-380-8	Sequence 8, Appli
4	64	97.0	18	2 US-08-475-055-8	Sequence 8, Appli
5	64	97.0	20	1 US-07-755-161A-3	Sequence 3, Appli
6	64	97.0	20	1 US-07-891-174-3	Sequence 3, Appli
7	64	97.0	20	1 US-08-204-487-1	Sequence 1, Appli
8	64	97.0	20	1 US-08-256-771-24	Sequence 24, Appli
9	64	97.0	20	1 US-08-381-984-25	Sequence 25, Appli
10	64	97.0	20	1 US-08-381-984-25	Sequence 24, Appli
11	64	97.0	20	1 US-08-381-984-25	Sequence 25, Appli
12	64	97.0	22	4 US-09-508-734-4	Sequence 4, Appli
13	64	97.0	24	4 US-09-508-734-6	Sequence 6, Appli
14	64	97.0	25	1 US-07-755-161A-10	Sequence 10, Appli
15	64	97.0	25	1 US-07-891-174-10	Sequence 10, Appli
16	64	97.0	25	1 US-08-204-487-7	Sequence 7, Appli
17	64	97.0	29	4 US-09-508-734-8	Sequence 8, Appli
18	64	97.0	36	1 US-07-755-161A-8	Sequence 8, Appli
19	64	97.0	36	1 US-07-891-174-8	Sequence 8, Appli
20	64	97.0	36	1 US-08-256-771-30	Sequence 30, Appli
21	64	97.0	36	1 US-08-381-984-29	Sequence 29, Appli
22	64	97.0	47	2 US-08-464-182A-6	Sequence 6, Appli
23	64	97.0	47	2 US-08-406-271-6	Sequence 6, Appli
24	64	97.0	50	2 US-08-693-274A-7	Sequence 7, Appli
25	64	97.0	52	4 US-09-017-043A-3	Sequence 3, Appli
26	64	97.0	53	2 US-08-464-182A-5	Sequence 5, Appli
27	64	97.0	53	2 US-08-406-271-5	Sequence 5, Appli

28	64	97.0	54	2 US-08-464-182A-2	Sequence 2, Appli
29	64	97.0	54	2 US-08-406-271-2	Sequence 2, Appli
30	64	97.0	594	3 US-08-724-586-2	Sequence 2, Appli
31	64	97.0	594	4 US-09-421-632-2	Sequence 2, Appli
32	64	97.0	594	4 US-09-932-190-2	Sequence 2, Appli
33	64	97.0	705	2 US-08-655-640-2	Sequence 2, Appli
34	64	97.0	708	2 US-08-655-640-4	Sequence 4, Appli
35	64	97.0	711	1 US-08-154-019-4	Sequence 4, Appli
36	64	97.0	711	1 US-08-461-333-4	Sequence 4, Appli
37	64	97.0	711	3 US-08-464-167-4	Sequence 4, Appli
38	64	97.0	711	3 US-09-158-313-4	Sequence 4, Appli
39	64	97.0	711	4 US-08-476-798-4	Sequence 4, Appli
40	61	92.4	711	1 US-08-145-681-2	Sequence 2, Appli
41	61	92.4	711	1 US-08-250-308-2	Sequence 2, Appli
42	61	92.4	711	1 US-08-453-703-2	Sequence 2, Appli
43	61	92.4	711	2 US-08-456-106-2	Sequence 2, Appli
44	61	92.4	711	3 US-08-456-108-2	Sequence 2, Appli
45	61	92.4	711	4 US-09-263-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAKOI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THIBEAULT
; ADDRESS: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FUN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 97.0%; Score 64; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQXMKVR 12
| | | | | | | | | |
Db 1 CFQWQXMKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485-948
FILING DATE: 26,742
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: peptide
DESCRIPTION: LF-Cl, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-485-948-8

Query Match 97.0%; Score 64; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQXMKVR 12
| | | | | | | | | |
Db 1 CFQWQXMKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5893441
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: peptide
DESCRIPTION: LF-Cl, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-628-380-8

Query Match 97.0%; Score 64; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQXMKVR 12
| | | | | | | | | |
Db 1 CFQWQXMKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5862245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475,055
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/485,948
;; FILING DATE:
;; APPLICATION NUMBER: 08/488,217
;; FILING DATE: JUNE 7, 1995
;; APPLICATION NUMBER: 08/418,642
;; FILING DATE: APRIL 7, 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 947-1-008A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; DESCRIPTION: LF-Cl, 8-25
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
JS-08-475-055-8

Query Match 97.0%; Score 64; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2y 1 CFQWQRXMRKVR 12
|||||
2b 1 CFQWQRXMRKVR 12

RESULT 5
JS-07-755-161A-3
; Sequence 3, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: DisplayWrite
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/755,161A
;; FILING DATE: 19910905
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX: 202-371-8856
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 2
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 19"
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 19
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 2"
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 97.0%; Score 64; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRXMRKVR 12
Db 2 CFQWRXMRKVR 13

RESULT 6
US-07-891-174-3
Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 23-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRXMRKVR 12
Db 2 CFQWRXMRKVR 13

RESULT 7
US-08-204-487-1
Sequence 1, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSIAKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSER: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1-20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 CFQWRXMRKVR 12
||| ||| ||| |||
Db 2 CFQWRXMRKVR 13

RESULT 8
US-08-256-771-24
Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
disulfide bond"

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 CFQWRXMRKVR 12
||| ||| ||| |||
Db 2 CFQWRXMRKVR 13

RESULT 10
US-08-381-984-24

US-08-256-771-24

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 CFQWRXMRKVR 12
||| ||| ||| |||
Db 2 CFQWRXMRKVR 13

RESULT 9
US-08-256-771-25
Sequence 25, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
prevent disulfide bond"

US-08-256-771-25

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 CFQWRXMRKVR 12
||| ||| ||| |||
Db 2 CFQWRXMRKVR 13

```
; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
;
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"
;
; US-08-381-984-24
;
; Query Match 97.0%; Score 64; DB 1; Length 20;
; Best Local Similarity 91.7%; Pred. No. 4.2e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 CFQWQRMKVR 12
; DB 2 CFQWQRMKVR 13
;
; RESULT 11
; US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
;
; US-09-743-107b-89
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Sanyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KE99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KRI998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4
;
; Query Match 97.0%; Score 64; DB 1; Length 20;
; Best Local Similarity 91.7%; Pred. No. 4.2e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 CFQWQRMKVR 12
; DB 2 CFQWQRMKVR 13
;
; RESULT 12
; US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Sanyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KE99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KRI998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4
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; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
JS-09-508-734-4
Query Match          97.0%; Score 64; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 4.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2Y 1 CFQWQRMKRVK 12
   |||||
db 2 CFQWQRMKRVK 13

RESULT 13
JS-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
JS-09-508-734-6

Query Match          97.0%; Score 64; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2Y 1 CFQWQRMKRVK 12
   |||||
db 3 CFQWQRMKRVK 14

RESULT 14
JS-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Menderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500KB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-755-161A-10

Query Match          97.0%; Score 64; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 5.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKRVK 12
   |||||
Db 4 CFQWQRMKRVK 15
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RESULT 15
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891.174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 08:08:15 ; Search time 6.88372 Seconds
(without alignments)
54.162 Million cell updates/sec

Title: US-09-743-107b-89
Perfect score: 66
Sequence: 1 CFQWQYMRKVR 12

Scoring table: BLOSUM62

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	64	97.0	15	9	US-09-798-869-2
2	64	97.0	25	9	US-09-798-869-20
3	64	97.0	694	9	US-10-023-096-2
4	56	84.8	15	9	US-09-798-869-6
5	53	80.3	15	9	US-09-798-869-3
6	53	80.3	25	9	US-09-798-869-23
7	45	68.2	15	9	US-09-798-869-7
8	44	66.7	15	9	US-09-798-869-4
9	44	66.7	25	9	US-09-798-869-22
10	41	62.1	15	9	US-09-798-869-8
11	41	62.1	15	9	US-09-798-869-29
12	41	62.1	15	9	US-09-798-869-30
13	37	56.1	10	10	US-09-864-761-47985
14	37	56.1	489	9	US-09-888-320-2
15	36	54.5	209	10	US-09-904-536-8
16	36	54.5	209	10	US-09-904-536-9
17	36	54.5	209	10	US-09-904-536-11
18	36	54.5	209	10	US-09-904-536-12
19	36	54.5	209	10	US-09-904-536-13

20	36	54.5	209	10	US-09-904-536-14	Sequence 14, Appl
21	36	54.5	209	10	US-09-904-536-15	Sequence 15, Appl
22	36	54.5	209	10	US-09-904-536-16	Sequence 16, Appl
23	36	54.5	209	10	US-09-904-536-17	Sequence 17, Appl
24	36	54.5	209	10	US-09-904-536-18	Sequence 18, Appl
25	36	54.5	212	10	US-09-904-536-10	Sequence 10, Appl
26	36	54.5	235	9	US-10-095-449-6	Sequence 6, Appl
27	36	54.5	235	10	US-09-448-378-1	Sequence 1, Appl
28	36	54.5	235	10	US-09-983-806-6	Sequence 6, Appl
29	36	54.5	235	10	US-09-904-536-1	Sequence 1, Appl
30	35	53.0	86	9	US-09-738-626-5715	Sequence 5715, Ap
31	34	51.5	95	10	US-09-764-864-1031	Sequence 1031, Ap
32	34	51.5	846	9	US-10-051-409-4	Sequence 4, Appl
33	34	51.5	1617	9	US-10-090-453A-2	Sequence 2, Appl
34	33	50.0	15	9	US-09-798-869-5	Sequence 5, Appl
35	33	50.0	46	10	US-09-864-761-48879	Sequence 48879, A
36	33	50.0	579	10	US-09-824-588-2	Sequence 2, Appl
37	32.5	49.2	124	10	US-09-864-761-44327	Sequence 44327, A
38	32	48.5	13	9	US-09-798-869-26	Sequence 26, Appl
39	32	48.5	14	9	US-09-798-869-25	Sequence 25, Appl
40	32	48.5	15	9	US-09-798-869-1	Sequence 1, Appl
41	32	48.5	15	9	US-09-798-869-10	Sequence 10, Appl
42	32	48.5	15	9	US-09-798-869-28	Sequence 28, Appl
43	32	48.5	18	9	US-09-798-869-24	Sequence 24, Appl
44	32	48.5	25	9	US-09-798-869-21	Sequence 21, Appl
45	32	48.5	25	10	US-09-909-652-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2
Query Match 97.0%; Score 64; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 2.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CFQWQYMRKVR 12
Db 3 CFQWQYMRKVR 14
RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON

APPLICANT: LARS VORLAND;
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match 97.0%; Score 64; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 4;le-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
| | | | | | | | | |
Db 3 CFQWQRMKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-023-096-2

Query Match 97.0%; Score 64; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.00096;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
| | | | | | | | | |
Db 22 CFQWQRMKVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match 84.8%; Score 56; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.00062;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
| | | | | | | | | |
Db 3 CFQWQRMKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

Query Match 80.3%; Score 53; DB 9; Length 15;
Best Local Similarity 72.7%; Pred. No. 0.0021;

Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

cy 1 CFQWQRMKRV 11
|:|||||:
db 3 CYQWQRMKRL 13

RESULT 6

US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINEBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 80.3%; Score 53; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 0.0034;
Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

cy 1 CFQWQRMKRV 11
|:|||||:
db 3 CYQWQRMKRL 13

RESULT 7

US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINEBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)

S-09-798-869-7

Query Match 58.2%; Score 45; DB 9; Length 15;
Best Local Similarity 53.8%; Pred. No. 0.051;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

cy 1 CFQWQRMKRV 11
|:|||||:
db 3 CYQWQRMKRL 13

RESULT 8

US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINEBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 66.7%; Score 44; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.077;
Matches 7; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

cy 1 CFQWQRMKRV 11
|:|||||:
db 3 CLRQWQRMKRV 13

RESULT 9

US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINEBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 66.7%; Score 44; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.12;
Matches 7; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

cy 1 CFQWQRMKRV 11
|:|||||:
db 3 CLRQWQRMKRV 13

RESULT 10

US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8

Query Match 62.1%; Score 41; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.26;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQXRMRKV 11
| 1 | 1 | 1 | 1 | 1 |
Db 3 CLRQWEMRKV 13

RESULT 11

US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 62.1%; Score 41; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.26;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQXRMRKV 11
| 1 | 1 | 1 | 1 | 1 |
Db 3 CFRQWEMKKL 13

RESULT 12

US-09-798-869-30

; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30

Query Match 62.1%; Score 41; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.26;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQXRMRKV 11
| 1 | 1 | 1 | 1 | 1 |
Db 3 CFRQWEMKKL 13

RESULT 13

US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: 2001-05-23
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 47985
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Homo sapiens

;; FEATURE:
;; OTHER INFORMATION: MAP TO AL096701.14
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
;; OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUATE 1.00e-06
IS-09-864-761-47985

Query Match 56.1%; Score 37; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQR 6
| | | | |
Db 16 CFQWRR 21

RESULT 14
IS-09-888-320-2
Sequence 2, Application US/09888320
Publication No. US20030013090A1
GENERAL INFORMATION:
;; APPLICANT: Barry III, Clifton E.
;; APPLICANT: DeBarber, Andrea E.
;; APPLICANT: Mdiluli, Khisimuzi
;; APPLICANT: Bekker, Linda-Gail
;; APPLICANT: The Government of the United States of America
;; APPLICANT: as represented by The Secretary of the
;; APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REFERENCE: 015280-413100US
CURRENT APPLICATION NUMBER: US/09/888,320
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 489
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: wild-type EtAa monooxygenase (Rv3854c, EthA)
IS-09-888-320-2

Query Match 56.1%; Score 37; DB 9; Length 489;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRXMRKV 11
| | | | |
Db 253 CQWPRRMRKM 263

RESULT 15
IS-09-904-536-8
Sequence 8, Application US/09904536
Patent No. US20020111475A1
GENERAL INFORMATION:

;; APPLICANT: Graddis, Thomas J.
;; APPLICANT: McGrew, Jeffrey T.
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
;; FILE REFERENCE: 03260.0028
;; CURRENT APPLICATION NUMBER: US/09/904,536
;; CURRENT FILING DATE: 2001-07-16
;; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
;; PRIOR FILING DATE: 1999-07-02
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 8
;; LENGTH: 209
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-904-536-8

Query Match 54.5%; Score 36; DB 10; Length 209;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRXMRK 10
| | | | |
Db 178 CLHWQTRRR 187

Search completed: February 21, 2003, 08:11:55
Job time : 6.88372 secs

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DM protein - protein search, using sw model

Run on: February 21, 2003, 07:48:01 ; Search time 10,6047 Seconds
(without alignments)
108,784 Million cell updates/sec

Title: US-09-743-107B-89

Perfect score: 66

Sequence: 1 CFQWQRXMRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	64	97.0	711	1 TFHUL	lactotransferrin p
2	53	80.3	708	2 JC22323	lactoferrin - goat
3	50	75.8	33	2 S52107	lactoferrin - shee
4	44	66.7	707	1 A28438	lactoferrin precu
5	43	65.2	4568	2 T08030	dyslein beta heavy
6	40	60.6	275	2 T22597	hypothetical prote
7	40	60.6	932	2 T28820	hypothetical prote
8	39	59.1	206	2 H97451	pyridoxamine 5'-ph
9	39	59.1	206	2 AB2670	pyridoxamine 5'-ph
10	39	59.1	208	2 AG3441	probable pyridoxam
11	38	57.6	289	2 G86403	33.3K hypothetical
12	38	57.6	515	2 T00510	probable cytochrom
13	38	57.6	543	2 T00513	cytochrome P450 ho
14	38	57.6	1135	2 T14803	phytochrome C - so
15	37	56.1	85	2 AG0794	polymyxin B resist
16	37	56.1	121	2 AH3147	hypothetical prote
17	37	56.1	255	2 E87515	signal peptidase I
18	37	56.1	433	2 T32605	hypothetical prote
19	37	56.1	489	2 C70555	probable monooxyge
20	37	56.1	584	2 C84325	hypothetical prote
21	36	54.5	235	2 I38440	flt3 ligand - huma
22	36	54.5	275	1 JC1113	interleukin-2 rece
23	36	54.5	275	1 S07442	interleukin-2 rece
24	36	54.5	456	2 C86624	hypothetical prote
25	36	54.5	456	2 H72000	hypothetical prote
26	36	54.5	1391	2 T20642	hypothetical prote
27	36	54.5	1397	2 E87988	protein F09C3.1 [h
28	35	53.0	124	2 C96582	Fls11.22 [imported
29	35	53.0	220	1 S36092	pyridoxamine-phosp

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N;Alternate names: lactoferrin

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C;Accession: G01394; S11228; A45401; S10324; S15953; S20841; S07160; A61169; A31000; S74

R;Cho. Y.

Submitted to the EMBL Data Library, March 1994

A;Reference number: G08620

A;Accession: G01394

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-711 <CHO>

A;Cross-references: EMBL:U07643; NID:G467236; PIDN:AB60324.1; PID:G467237

R;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A;Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A;Reference number: S11228; MUID:90384839; PMID:2402455

A;Accession: S11228

A;Molecule type: mRNA

A;Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A;Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R;Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A;Title: Differential molecular mechanism of the estrogen action that regulates lactofer

A;Reference number: A45401; MUID:93125571; PMID:1480183

A;Accession: A45401

A;Molecule type: DNA

A;Residues: 1-15 <TEN>

A;Cross-references: GB:S52659; NID:G263311; PIDN:AB24877.1; PID:G263312

A;Experimental source: placenta

A;Note: sequence extracted from NCBI backbone (NCBIP:122202)

R;Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A;Title: Nucleotide sequence of human lactoferrin cDNA.

A;Reference number: S10324; MUID:90326549; PMID:2374734

A;Accession: S10324

A;Molecule type: mRNA

A;Residues: 3-711 <POW>

A;Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R;Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A;Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A;Reference number: S15853; MUID:91264786; PMID:2049066

A;Accession: S15853

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 20-31 <ST1>

A;Accession: S20841

A;Molecule type: Protein

A;Residues: 20-28, 'X', 30-31 <ST2>

A;Residues: 20-28, 'X', 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A;Reference number: S07160; MUID:88001031; PMID:3477300
 A;Accession: S07160
 A;Molecule type: mRNA
 A;Residues: 436-487, 'A', 489-711 <RAD>
 A;Cross-references: EMBL:M18642; NID:g186615; PIDN:AAA86665.1; PID:g386855
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A;Reference number: A61169; MUID:91235214; PMID:1674448
 A;Accession: A61169
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 3701, SWKPVN' <PAN>
 A;Experimental source: normal breast tissue
 R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
 Eur. J. Biochem. 145, 659-666, 1984
 A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
 A;Reference number: A31000; MUID:85076667; PMID:6510420
 A;Accession: A31000
 A;Molecule type: protein
 A;Residues: 20-140,142-169,171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
 A;Note: this is the final paper in a series
 R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity
 A;Reference number: S74119; MUID:97054624; PMID:8898921
 A;Accession: S74119
 A;Molecule type: protein
 A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A;Experimental source: neutrophil granulocytes
 C;Genetics:
 A;Gene: GDB:LTF
 A;Cross-references: GDB:119368; OMIM:150210
 A;Map position: 3q21-3q23
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein; iron binding; milk
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-711/Product: lactotransferrin #status experimental <MAT>
 F;21-356/Domain: transferrin repeat homology <TRH1>
 F;360-699/Domain: transferrin repeat homology <TRH2>
 F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
 F;37-498/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat

Query Match 97.0%; Score 64; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.0083;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRMKRV 12
 Db 39 CFQWQRMKRV 50

RESULT 2
 JC2323
 lactoferrin - goat
 C;Species: Capra aegagrus hircus (domestic goat)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C;Accession: JC2323
 R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A;Reference number: JC2323; MUID:94380047; PMID:8093048
 A;Accession: JC2323
 A;Molecule type: mRNA
 A;Residues: 1-708 <LEP>
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; transferrin; glycoprotein
 F;359-696/Domain: transferrin repeat homology <TRH2>
 F;252,300,378,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.3%; Score 53; DB 2; Length 708;
 Best Local Similarity 72.7%; Pred. No. 0.083;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRMKRV 11
 Db 38 CYQWQRMKRL 48

RESULT 3
 S52107
 lactoferrin - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
 C;Accession: S52107
 R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
 Biochim. Biophys. Acta 1243, 25-32, 1995
 A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet
 A;Reference number: S52107; MUID:95127729; PMID:7827104
 A;Accession: S52107
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-33 <QIA>
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication
 Query Match 75.8%; Score 50; DB 2; Length 33;
 Best Local Similarity 63.6%; Pred. No. 0.016;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRMKRV 11
 Db 19 CYQWQRMKRL 29

RESULT 4
 A28438
 lactoferrin precursor - mouse
 N;Alternate names: lactotransferrin
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A28438; A41205
 R;Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
 A;Reference number: A32596; MUID:87280033; PMID:3611056
 A;Accession: A28438
 A;Molecule type: mRNA
 A;Residues: 3-707 <PEN>
 A;Cross-references: EMBL:J03298
 R;Liu, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A;Reference number: A41205; MUID:92042099; PMID:1939212
 A;Accession: A41205
 A;Molecule type: DNA
 A;Residues: 1-15 <LIU>
 A;Cross-references: GB:M74778
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-707/Product: lactotransferrin #status predicted <MAT>
 F;358-695/Domain: transferrin repeat homology <TRH2>
 F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.7%; Score 44; DB 1; Length 707;
 Best Local Similarity 63.6%; Pred. No. 3.6;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQRMKRV 11
 Db 37 CLRQWQRMKRV 47

```

ESULT 5
y:in beta heavy chain - Chlamydomonas reinhardtii
;Species: Chlamydomonas reinhardtii
;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
;Accession: T08030
;Mittchell, D.R.; Brown, K.S.
;Cell Sci. 107, 635-644, 1994
;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
;Reference number: Z16302; PMID:94274778; PMID:8006077
;Accession: T08030
;Status: translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-4568 <MIT>
;Cross-references: EMBL:U02963; NID:G409965; PIDN:AAA19956.1; PID:G514215
;Experimental source: strain 21gr
;Genetics:
;Gene: ODA4
;Map position: IX
;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
3334/3; 3686/3; 3882/3; 4240/3
;Superfamily: dynein heavy chain, ciliary
;Keywords: nucleotide binding, P-loop
;1919-1948/Region: nucleotide-binding motif A (P-loop)
;2202-2209/Region: nucleotide-binding motif A (P-loop)
;2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 65.2%; Score 43; DB 2; Length 4568;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

y 1 CFQQRXMRKVR 12
||||| : :
b 1852 CFQWSQLRYIQ 1863

ESULT 6
22597
y:pothetical protein F53H4.4 - Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
;Accession: T22597
;Dobson, R.
;Submitted to the EMBL Data Library, October 1996
;Reference number: Z19587
;Accession: T22597
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-275 <WIL>
;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GNO00028; CESP:F53H4.4
;Experimental source: clone F53H4
;Genetics:
;Gene: CESP:F53H4.4
;Map position: X
;Introns: 67/1; 153/1
;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4

Query Match 60.8%; Score 40; DB 2; Length 275;
Best Local Similarity 63.6%; Pred. No. 7.8;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

y 2 FQWRXMRKVR 12
||||| : :
b 262 FQWISMRKTR 272

ESULT 7
28820
y:pothetical protein F07C3.1 - Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T28820
R;Ravello, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A;Description: the sequence of C. elegans cosmid F07C3.
A;Reference number: Z20528
A;Accession: T28820
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-932 <FAV>
A;Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GNO00023; CESP:F07C3.1
A;Experimental source: strain Bristol N2; clone F07C3
C;Genetics:
A;Gene: CESP:F07C3.1
A;Map position: 5
A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599

Query Match 60.6%; Score 40; DB 2; Length 932;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FQWRXMRKVR 12
||||| : :
Db 579 FQWRSARLVK 589

RESULT 8
H97451
pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (str
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: H97451
R;Gaudier, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum-
A;Reference number: A97359; PMID:11743194
A;Accession: H97451
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK96569.1; PID:gl5155733; GSPDB:GNO00169
C;Genetics:
A;Gene: AGR_C 1381
A;Map position: circular chromosome
C;Superfamily: pyridoxamine-phosphate oxidase

Query Match 59.1%; Score 39; DB 2; Length 206;
Best Local Similarity 50.0%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWRXMRKVR 12
||||| : :
Db 88 CFHWKSLRRQVR 99

RESULT 9
AB2670
pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Du
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AB2670
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillat, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AB2670
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <KUR>

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A;Cross-references: GB:AB008688; PID:17739129; GSPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: pmxH
 C;Superfamily: pyridoxamine-phosphate oxidase

Query Match 59.1%; Score 39; DB 2; Length 206;
 Best Local Similarity 50.0%; Pred. No. 9;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
 |||:|:
 Db 88 CFHWKSLRQVR 99

RESULT 10
 33-3K hypothetical protein F28L5.13 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 01-Feb-2002 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
 C;Accession: G86403
 R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 C;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: G86403
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-289 <STO>
 A;Cross-references: GB:AE005172; NID:g10998925; PIDN:AAG26065.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1

Query Match 59.1%; Score 39; DB 2; Length 208;
 Best Local Similarity 50.0%; Pred. No. 9;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
 |||:|:
 Db 90 CFHWKSLRQVR 101

RESULT 11
 33-3K hypothetical protein F28L5.13 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
 C;Accession: G86403
 R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 C;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: G86403
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-289 <STO>
 A;Cross-references: GB:AE005172; NID:g10998925; PIDN:AAG26065.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1

Query Match 57.6%; Score 38; DB 2; Length 289;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
 |||:|:
 Db 8 CFTWEEYARHVR 19

RESULT 12
 T00510
 probable cytochrome P450 At2g23220 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
 C;Accession: T00510; A84622
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, submitted to the EMBL Data Library, November 1997
 A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
 A;Reference number: Z14164
 A;Accession: T00510
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-515 <ROU>
 A;Cross-references: EMBL:AC002391; NID:G2642427; PID:G2642441
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: A84622
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-515 <STO>
 A;Cross-references: GB:AE002093; NID:G2642441; PIDN:AA87109.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g23220; T20D16.15
 A;Map position: 2
 A;Introns: 182/3; 310/3
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: heme; iron; metalloprotein
 F;312-471/Domain: cytochrome P450 homology <P45>
 F;449/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 57.6%; Score 38; DB 2; Length 515;
 Best Local Similarity 83.3%; Pred. No. 33;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 6
 |||:|:
 Db 469 CFQWQXMRKVR 474

RESULT 13
 T00513
 cytochrome P450 homolog At2g23190 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
 C;Accession: T00513; F84621
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, submitted to the EMBL Data Library, November 1997
 A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
 A;Reference number: Z14164
 A;Accession: T00513
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-543 <ROU>
 A;Cross-references: EMBL:AC002391; NID:G2642427; PID:G2642444
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84621
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-543 <S>
A;Cross-references: GB:AE002093; NID:G2642444; PIDN:AB87112.1; GSPDB:GN00139
A;Gene: pmrD
A;Map position: 2
A;Introns: 211/3; 339/3
A;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
A;Keywords: heme; iron; metalloprotein
A;341-500/Domain: cytochrome P450 homology <P45>
A;478/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 57.6%; Score 38; DB 2; Length 543;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CFOWOR 6
| | | | |
b 498 CFOWOR 503

RESULT 14
14803
phytochrome C - sorghum
A;Species: Sorghum bicolor (sorghum)
A;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
A;Accession: T14803
A;Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet,
submitted to the EMBL Data Library, April 1996
A;Reference number: Z18186
A;Accession: T14803
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1135 <CHI>
A;Cross-references: EMBL:U56731; NID:G1800218; PID:G1800219
A;Gene: PHYC
A;Superfamily: phytochrome; phytochrome homology
A;Keywords: chromoprotein; dimer; photoreceptor; phytochromobilin; transcription regulat
A;65-581/Domain: phytochrome homology <PHY>
A;321/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 57.6%; Score 38; DB 2; Length 1135;
Best Local Similarity 36.4%; Pred. No. 69;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Y 1 CFOWORXMRKV 11
| | | | |
b 775 CLEWKAQKI 785

RESULT 15
AG0794
polymyxin B resistance protein [imported] - *Salmonella enterica* subsp. *enterica* serovar
A;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A;Note: this species has also been called *Salmonella typhi*
A;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
A;Accession: AG0794
A;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
h. T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
ature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AG0794
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-85 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07537.1; PID:G16503529; GSPDB:GN00176
A;Genetics:
A;Gene: pmrD
Query Match 56.1%; Score 37; DB 2; Length 85;
Best Local Similarity 60.0%; Pred. No. 8.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFOWORXMRK 10
| | | | |
Db 74 CDEWQRLTRK 83

Search completed: February 21, 2003, 08:02:44
Job time : 10.6047 secs

GenCore version 5.1.3
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M protein - protein search, using sw model

run on: February 21, 2003, 07:28:06 ; Search time 5.2093 Seconds
(without alignments)
95.544 Million cell updates/sec

title: US-09-743-107B-89

effect score: 66

sequence: 1 CFQWQKXKVR 12

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 112892 seqs, 41476328 residues

total number of hits satisfying chosen parameters: 112892

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	64	97.0	711	1 TRFL_HUMAN	P02788 homo sapien
2	53	80.3	708	1 TRFL_CAMDR	Q9tun0 camelus dro
3	53	80.3	708	1 TRFL_CAPHI	Q29477 capra hircu
4	44	66.7	707	1 TRFL_MOUSE	P08071 mus musculu
5	43	65.2	4568	1 DYHB_CHLRE	Q39565 chlamydomon
6	39	59.1	695	1 TRFL_HORSE	O77811 equus cabal
7	38	57.6	292	1 NLA_DROME	O9xz18 drosophila
8	38	57.6	1135	1 PHVC_SORBI	P93528 sorghum bic
9	37	56.1	185	1 PMRD_SALTY	P37589 salmonella
10	37	56.1	146	1 RPOB_LIBAF	P41187 liberibacte
11	36	54.5	235	1 FL3L_HUMAN	P49771 homo sapien
12	36	54.5	275	1 IL2A_BOVIN	P12342 bos taurus
13	36	54.5	275	1 IL2A_SHEEP	P26898 ovis aries
14	36	54.5	1137	1 PHVC_ORYSA	O92w19 oryza sativ
15	36	54.5	1179	1 ATK1_ARATH	Q91t02 arabidopsis
16	35	53.0	270	1 PDHX_MYXXA	P21159 myxococcus
17	35	53.0	306	1 BUS2_YEAST	P26448 saccharomyc
18	35	53.0	435	1 DCOR_PANRE	P49725 panagrellus
19	35	53.0	502	1 C911_ARATH	Q9fg65 arabidopsis
20	35	53.0	783	1 YNR2_CAEEL	Q21988 caenorhabdi
21	35	53.0	2594	1 7LBS_DROVI	P20806 drosophila
22	34	51.5	211	1 LOLE_VIBCH	P57070 vibrio chol
23	34	51.5	227	1 CHEZ_PSEAE	Q51434 pseudomonas
24	34	51.5	275	1 VA16_VACCV	P16710 vaccinia vi
25	34	51.5	378	1 VA16_VACCC	P20993 vaccinia vi
26	34	51.5	455	1 RADA_CHLMU	Q9pk96 chlamydia m
27	34	51.5	500	1 TLCE_RICPR	O05962 rickettsia
28	34	51.5	708	1 TRFL_BUBBU	O77698 bubalus bub
29	34	51.5	765	1 Y008_HUMAN	Q15398 homo sapien
30	34	51.5	962	1 YBX7_SCHPO	Q10201 schizosacch
31	33	50.0	159	1 Y1CN_ECOLI	P31439 escherichia
32	33	50.0	272	1 IL2A_HUMAN	P01589 homo sapien
33	33	50.0	377	1 VA16_VARV	P33841 variola vir

ALIGNMENTS

RESULT 1
TRFL_HUMAN STANDARD; PRT; 711 AA.
ID TRFL_HUMAN Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96KZ4;
AC Q96KZ5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;
DE Lactoferrin B; Lactoferrin C].
GN LTF OR Lf.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90384339; PubMed=2402455;
RA Key M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RL Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Conneely O.M.;
RT Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang Q., Jimenez-Flores R., Richardson T.;
RT "Molecular cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RT "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cheng H., Chen X., Huan L.;
RT "cDNA cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]

34 33 50.0 428 1 SYH_CHLMU Q9pj9 chlamydia m
35 33 50.0 475 1 YBEA_HAEIN P4693 haemophilus
36 33 50.0 496 1 MGS1_SCHPO Qute7 schizosacch
37 33 50.0 506 1 AER_ECOLI P50466 escherichia
38 33 50.0 704 1 TRFL_PIG P14632 sus scrofa
39 33 50.0 1131 1 PHY_BINSY Q41045 pinus sylve
40 33 50.0 1213 1 T2D2_DROME Q24325 drosophila
41 33 50.0 1293 1 XPC_DROME Q24595 drosophila
42 33 50.0 2554 1 7LES_DROME P3368 drosophila
43 32 48.5 77 1 NULM_ASCSU P24874 ascaris suu
44 32 48.5 137 1 YEDD_ECOLI P31063 escherichia
45 32 48.5 141 1 YEDD_SALTY Q06399 salmonella

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE-Mammary gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.,
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RA Legrand D., Spik G., Montreuil J., Jolles P.,
RT "Human lactotransferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046917; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RA Jolles P.,
RT "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RN Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RA Jolles P.,
RT "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin.";
RL FEBS Lett. 142:107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.,
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giscalone J., Pease A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.,
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.,
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.,
RT "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.,
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253--methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.,
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.,
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.,
RT "Isolation and characterization of opiod antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
RA El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Heitmancik J.F., Teng C.T.,
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
RN [21]
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
RN [22]
RP FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
RN [23]
RP SUBUNIT: MONOMER.
CC
RN [24]
RP SUBCELLULAR LOCATION: Secreted.
CC
RN [25]
RP DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC
RN [26]
RP SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
RN [27]
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CC or send an email to license@isb-sib.ch).
RN [28]
RP EMBL; X53961; CAA37914.1; -
CC
RN [29]
RP EMBL; U07643; AAB60324.1; -
CC
RN [30]
RP EMBL; M93150; AAA36159.1; -
CC
RN [31]
RP EMBL; M83202; AAA59511.1; -
CC
RN [32]
RP EMBL; M83205; AAA58656.1; -
CC
RN [33]
RP EMBL; X18642; AAA86665.1; -
CC
RN [34]
RP EMBL; AF332168; AAG48753.1; -
CC
RN [35]
RP EMBL; BC015822; AAH15822.1; -
CC
RN [36]
RP EMBL; BC015823; AAH15823.1; -
CC
RN [37]
RP EMBL; M73700; AAA59479.1; -
CC
RN [38]
RP EMBL; X52941; CAA37116.1; -
CC
RN [39]
RP EMBL; U95626; AAB57795.1; -
CC
RN [40]
RP PIR; S11228; TFHUL.
CC
RN [41]
RP PDB; 1LFCF; 31-AUG-94.
CC
RN [42]
RP PDB; 1LCT; 31-OCT-93.
CC
RN [43]
RP PDB; 1LFG; 31-JUL-94.
CC
RN [44]
RP PDB; 1LFH; 31-OCT-93.
CC
RN [45]
RP PDB; 1LPI; 31-OCT-93.
CC
RN [46]
RP PDB; 1LGB; 31-AUG-94.
CC
RN [47]
RP PDB; 1LGC; 31-AUG-94.
CC
RN [48]
RP PDB; 1BKA; 08-NOV-96.
CC
RN [49]
RP PDB; 1DSN; 08-MAR-96.
CC
RN [50]
RP PDB; 1HSE; 12-MAR-97.
CC
RN [51]
RP PDB; 1VFD; 21-APR-97.
CC

Query Match 97.0%; Score 64; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00024;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQWQRMKVR 12
 b 39 CFQWQRMKVR 50

RESULT 2

RFL CAMDR
 D TRFL CAMDR STANDARD; PRT; 708 AA.
 C Q3TMQ; Q9MZS5;
 T 16-OCT-2001 (Rel. 40, Created)
 T 16-JUN-2001 (Rel. 40, Last sequence update)
 T 15-JUN-2002 (Rel. 41, Last annotation update)
 E Lactotransferrin precursor (Lactoferrin).
 N LTF.
 S Camelus dromedarius (Dromedary) (Arabic camel).
 C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 X Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 N NCBI_TaxID=9838;
 [1]
 P SEQUENCE FROM N.A.
 C STRAIN=Somali; TISSUE=Lactating mammary gland;
 A Kappeler S.R., Ackermann M., Farah Z., Puhon Z.;
 T "Sequence analysis of camel (Camelus dromedarius) lactoferrin."
 L Int. Dairy J. 9:481-486 (1999).
 N [2]
 P SEQUENCE FROM N.A.
 C TISSUE=Mammary gland;
 A Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 L Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 C -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 C -1- SUBUNIT: MONOMER (BY SIMILARITY).
 C -1- SUBCELLULAR LOCATION: Secreted.
 C -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 C -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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R EMBL; AJ131674; CAB53387.1; -;
 R EMBL; AF165879; AAF82241.1; -;
 R HSSP; O77811; 1B1X.
 R InterPro; IPR001156; Transferrin.
 R Pfam; PF00405; transferrin; 2.
 R PRINTS; PR00422; TRANSFERRIN.
 R SMART; SM00094; TFF; 2.
 R PROSITE; PS00205; TRANSFERRIN_1; 2.
 R PROSITE; PS00206; TRANSFERRIN_2; 2.
 R PROSITE; PS00207; TRANSFERRIN_3; 2.
 W Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 W Signal.
 T CHAIN 1 19 BY SIMILARITY.
 T CHAIN 20 708 LACTOTRANSFERRIN.
 T REPEAT 20 363 1.
 T REPEAT 364 708 2.
 T DISULFID 28 64 BY SIMILARITY.
 T DISULFID 38 55 BY SIMILARITY.
 T DISULFID 134 217 BY SIMILARITY.
 T DISULFID 176 192 BY SIMILARITY.
 T DISULFID 189 200 BY SIMILARITY.
 T DISULFID 250 264 BY SIMILARITY.
 T DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79 IRON 1 (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 261 261 F -> S (IN REF. 2).
 FT CONFLICT 304 304 G -> A (IN REF. 2).
 FT CONFLICT 330 330 S -> P (IN REF. 2).
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
 FT CONFLICT 506 506 L -> F (IN REF. 2).
 FT CONFLICT 609 609 A -> P (IN REF. 2).
 FT CONFLICT 642 642 R -> Q (IN REF. 2).
 SQ SEQUENCE 708 AA; 77211 MW; 080C175A0B69D430 CRC64;

Query Match 80.3%; Score 53; DB 1; Length 708;
 Best Local Similarity 75.0%; Pred. No. 0.025;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
 DB 38 CAQWQRMKVR 49

RESULT 3

TRFL CAPHI STANDARD; PRT; 708 AA.
 ID Q29477; Q29479;
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OC NCBI_TaxID=9925;
 RN (1)_TaxID=9925;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=94380047; PubMed=8093048;
 RA le Provost F., Nocart M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 relevant locus to bovine UI2 syntenic group."
 RL Biochem. Biophys. Res. Commun. 203:1324-1332 (1994).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.

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 DR EMBL; AJ010930; CAA09407.1; --
 DR PDB; 1BIX; 02-DEC-98.
 DR PDB; 1B7U; 02-FEB-99.
 DR PDB; 1B7Z; 02-FEB-99.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PRO0422; TRANSFERRIN.
 DR SMART; SM00094; TR FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN 1; 2.
 DR PROSITE; PS00206; TRANSFERRIN 2; 1.
 DR PROSITE; PS00207; TRANSFERRIN 3; 1.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 FT SIGNAL; 3D-structure. 1
 FT NON TER 1
 FT SIGNAL <1 6
 FT CHAIN 7 695 LACTOTRANSFERRIN.
 FT REPEAT 7 350
 FT REPEAT 351 695
 FT DISULFID 15 41
 FT DISULFID 25 42
 FT DISULFID 121 204
 FT DISULFID 163 179
 FT DISULFID 166 189
 FT DISULFID 176 187
 FT DISULFID 237 251
 FT DISULFID 354 386
 FT DISULFID 364 377
 FT DISULFID 411 690
 FT DISULFID 431 653
 FT DISULFID 463 538
 FT DISULFID 487 681
 FT DISULFID 497 511
 FT DISULFID 508 521
 FT DISULFID 579 593
 FT DISULFID 631 636
 FT METAL 66 66
 FT METAL 98 98
 FT METAL 138 138
 FT METAL 259 259
 FT METAL 401 401
 FT METAL 439 439
 FT METAL 532 532
 FT METAL 601 601
 FT METAL 127 127
 FT BINDING 127 127
 FT BINDING 469 469
 FT CARBOHYD 143 143 (POTENTIAL).
 FT CARBOHYD 287 287 (POTENTIAL).
 FT CARBOHYD 482 482 (POTENTIAL).
 SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

 Query Match 59.1%; Score 39; DB 1; Length 695;
 Best Local Similarity 58.3%; Pred. No. 9.3;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CFQWQRXMRKVR 12
 Db 25 CAKFORNMKVR 36

 RESULT 7
 NLA DROME
 AC Q9XZL8; Q9V391; PRT; 292 AA.
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Nebula protein.
 GN NLA OR CG6072.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP McCormick A.V., Goldberg M.L.;
 RA "Gene required for elongation of meiosis I spindle in Drosophila
 RT females.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaese R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotter P.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Center A., Chandra I.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Davenport L.B., Davies P.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fostek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang Q.A.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 CC The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
 CC -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.

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 DR EMBL; AF147700; AAD33987.1; --
 DR EMBL; AE03712; AAF55285.1; --
 DR Flybase; FBgn0026629; nla.
 SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F68A6CF9 CRC64;

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DR SMART; SMO0387; HATPaase C; 1.
DR SMART; SMO0388; HIsKA; 1.
DR SMART; SMO0086; PAC; 1.
DR SMART; SMO0091; PAS; 2.
DR TIGRFAMs; TIGR00229; sensory_box; 2.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50112; PAS; 2.
DR PROSITE; PS50245; PHYTOCHROME_1; FALSE_NEG.
DR PROSITE; PS50046; PHYTOCHROME_2; 1.
KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
KW Repeat; Multigene family.
FT DOMAIN 618 688 PAS 1.
FT DOMAIN 748 822 PAS 2.
FT DOMAIN 902 1122 HISTIDINE_KINASE.
FT BINDING 321 321 CHROMOPHORE (BY SIMILARITY).
SQ SEQUENCE 1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;

Query Match 57.6%; Score 38; DB 1; Length 1135;
Best Local Similarity 36.4%; Pred. No. 23;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRXMRKV 11
| : | : | :
DB 775 CLEWKNAMQKI 785

RESULT 9
PMRD_SALTY
ID PMRD SALTY STANDARD; PRT; 85 AA.
AC P37589;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Polymyxin B resistance protein pmrd.
GN PMRD-OR STM2304.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
NCBI_TaxID=602;
RN [1]
RX MEDLINE=94266712; PubMed=8206837;
RC STRAIN=LT2;
RC RC
RA Roland K.L., Esther C.R., Spitnagel J.K.;
RA "Isolation and characterization of a gene, pmrd, from Salmonella
RT typhimurium that confers resistance to polymyxin when expressed in
RT multiple copies."
RL J. Bacteriol. 176:3589-3597(1994).
RP SEQUENCE FROM N.A.
RX MEDLINE=94266712; PubMed=8206837;
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RC RC
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
CC -!- FUNCTION: CONFERS RESISTANCE TO POLYMYXIN B. POLYMYXIN RESISTANCE
CC MAY BE MEDIATED BY AN INTERACTION BETWEEN PMRA OR A PMRA-REGULATED
CC GENE PRODUCT AND PMRD.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U02281; AAA21322.1; -

```

DR EMBL; AE008803; AAL21205.1; -;
AC StyGene; SGI0304; pnrD.
KW Antibiotic resistance; Complete proteome.
SQ SEQUENCE 85 AA; 9749 MW; 1E1822419EA50CCA CRC64;

Query Match 56.1%; Score 37; DB 1; Length 85;
Best Local Similarity 60.0%; Pred. No. 2.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQXMRK 10
Db 74 CDWQLTRK 83

RESULT 10
RPOB LIBAF STANDARD; PRT; 146 AA.
AC P41187;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
DE beta chain) (RNA polymerase beta subunit) (Fragment).
GN RPOB.
OS Liberibacter africanus (Liberibacter africanum).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Candidatus Liberibacter.
OX NCBI_TaxID=34020;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nelepruit;
RA Planet P., Jaqueux S., Bove J.M., Garnier M.;
RT "Detection and characterization of the African Citrus Greening
RT Liberibacter by amplification, cloning and sequencing of the rplKAL-
RT rpoB operon.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
CC
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CC
CC EMBL; U09675; AAA19557.1; -;
DR InterPro; IPR001572; RNA pol_B.
DR Pfam; PF00562; RNA pol_B; 1.
DR PROSITE; PS01166; RNA POL BETA; PARTIAL.
KW Transferrase; Transcription; DNA-directed RNA polymerase.
FT NON TER 146
SQ SEQUENCE 146 AA; 16731 MW; 815D6EDD66FDB943 CRC64;

Query Match 56.1%; Score 37; DB 1; Length 146;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQXMRK 10
Db 10 CVQWQGRK 19

RESULT 11
FL3L HUMAN

ID FL3L HUMAN STANDARD; PRT; 235 AA.
AC P49771;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3
DE ligand) (Flt3L).
GN FLT3LG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195428; PubMed=8145851;
RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,
RA Duda G., Martina G., Peterson D., Menon S., Shanafelt A.,
RA Muench M., Kainer N., Namikawa R., Rennick D., Roncarolo M.G.,
RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
RT "Ligand for Flt3/Flk2 receptor tyrosine kinase regulates growth of
RT haematopoietic stem cells and is encoded by variant RNAs.";
RL Nature 368:643-648(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94235842; PubMed=8180375;
RA Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,
RA Escobar S.S., Downey H., Splet R.R., Beckmann M.P., McKenna H.J.;
RT "Cloning of the human homologue of the murine flt3 ligand: a growth
RT factor for early hematopoietic progenitor cells.";
RL Blood 83:2795-2801(1994).
RN [3]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=96032581; PubMed=7566977;
RA Lyman S.D., Stocking K., Davidson B., Fletcher F., Johnson L.,
RA Escobar S.;
RT "Structural analysis of human and murine flt3 ligand genomic loci.";
RL Oncogene 11:1165-1172(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=20343011; PubMed=10881197;
RA Savvides S.N., Boone T., Karplus P.A.;
RT "Flt3 ligand structure and unexpected commonalities of helical
RT bundles and cystine knots.";
RL Nat. Struct. Biol. 7:486-491(2000).
CC -!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
CC FACTORS AND INTERLEUKINS.
CC -!- SUBUNIT: Homodimer (isoform 2).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
CC secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here)
CC and 2/soluble; are produced by alternative splicing.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U04806; AAA17989.1; -;
DR EMBL; U03858; AAA19825.1; -;
DR EMBL; U29874; AAA90949.1; -;
DR EMBL; U29874; AAA90950.1; -;
DR PDB; 1ETE; 09-JUN-00.
DR Genew; HGNC:3766; FLT3LG.
DR MIM; 600007; -;
DR InterPro; IPR004213; Flt3 lig.
DR Pfam; PF02947; Flt3 lig; 1.
KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;
KW 3D-structure.

T SIGNAL 1 26
T CHAIN 27 235
T DOMAIN 27 184
T TRANSMEM 185 205
T DOMAIN 206 235
T DISULFID 30 111
T DISULFID 70 153
T DISULFID 119 158
T CARBOHYD 126 126
T CARBOHYD 149 149
T VARSPLIC 161 178
T VARSPLIC 179 235
T CONFLICT 72 72
T SEQUENCE 235 AA; 26416 MW; 73B95BF693B4CECF CRC64;
Q

Query Match 54.5%; Score 36; DB 1; Length 235;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Y 1 CFQWQXMRK 10
b 204 CLWQRTERR 213

RESULT 12
L2A BOVIN STANDARD; PRT; 275 AA.
C P12342;
T 01-OCT-1989 (Rel. 12, Created)
T 01-OCT-1989 (Rel. 12, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
E Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).
N IL2RA.
S Bos taurus (Bovine).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
C Bovidae; Bovinae; Bos.
X NCBI_TaxID=9913;
N [1]
P SEQUENCE FROM N.A.
X MEDLINE=88212503; PubMed=2835311;
A Weinberg A.D., Shaw J., Faekau V., Bleackley R.C., Magnuson N.S.,
T "Cloning and chromosomal assignment of the bovine interleukin-2 receptor alpha (IL-2R alpha) gene."
L Mamm. Genome 6:751-753(1995).
P [2]
P SEQUENCE OF 1-21 FROM N.A.
X MEDLINE=96116968; PubMed=85631178;
A Yoo J., de Leon F.A., Stone R.I., Beattie C.W.;
T "Cloning and chromosomal assignment of the bovine interleukin-2 receptor alpha (IL-2R alpha) gene."
L Mamm. Genome 6:751-753(1995).
P [1]
C -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
C EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE WITH A GAMMA CHAIN.
C -1- SUBCELLULAR LOCATION: Type I membrane protein.
C -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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R EMBL; M20818; AAA51414.1; --
R EMBL; U24226; AAC48487.1; --

DR PIR; S07442; S07442.
DR HSP; P01589; IILM.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 2.
DR SMART; SM00032; CCP; 2.
KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
FT SIGNAL 1 21
FT CHAIN 22 275
FT DOMAIN 22 243
FT TRANSMEM 244 252
FT DOMAIN 263 275
FT DOMAIN 23 78
FT DOMAIN 122 185
FT DISULFID 24 64
FT DISULFID 251 77
FT DISULFID 123 168
FT DISULFID 152 184
FT CARBOHYD 80 80
FT CARBOHYD 109 109
SQ SEQUENCE 275 AA; 31238 MW; 4901BBF9A4862390 CRC64;
Q

Query Match 54.5%; Score 36; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
Db 261 CLWQKWKXNR 272

RESULT 13
IL2A SHEEP STANDARD; PRT; 275 AA.
ID IL2A SHEEP
AC P26896;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).
GN IL2RA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
CX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RA Verhagen A.A.;
RN Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92241682; PubMed=1572550;
RA Bujdosó R., Sargan D.R., Williamson M.L., McConnell I.;
RT "Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa protein, CD25."
RL Gene 113:283-284(1992).
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE WITH A GAMMA CHAIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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R EMBL; M20818; AAA51414.1; --
R EMBL; U24226; AAC48487.1; --


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CC EMBL; Z11560; CAA77652.1; -
CC EMBL; X60149; CAA42723.1; -
CC EMBL; A19167; CAA01447.1; -
CC FIR; S18910; S18910.
CC FIR; S18899; S18899.
CC FIR; J01113; J01113.
CC HSP; P01589; I11M.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00084; sushi; 2.
CC SMART; SM00032; CCP; 2.
KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
FT SIGNAL 1 21
FT CHAIN 22 275
FT DOMAIN 22 243
FT TRANSMEM 244 262
FT DOMAIN 263 275
FT DOMAIN 23 78
FT DOMAIN 122 185
FT DISULFID 24 64
FT DISULFID 751 77
FT DISULFID 123 168
FT DISULFID 152 184
FT CARBOHYD 80 80
FT CONFLICT 166 166
FT SEQUENCE 275 AA; 30904 MW; 1101A2DE5ACSA088 CRC64;
Query Match 54.5%; Score 36; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 CFQWQRMKRV 12
DB 261 CLTWQRWKKQR 272
RESULT 14
PHYC_ORYSA STANDARD; PRT; 1137 AA.
AC Q9ZWI9; P93429;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome C.
GN PHYC.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Tahir M., Kanegae H., Takano M.;
RT "Phytochrome C (PHYC) gene in rice: isolation and characterization of
a complete coding sequence.";
RL (in) Plant Gene Register PGR98-210.
[2]
RP SEQUENCE OF 275-378 FROM N.A.
RX MEDLINE=97019052; PubMed=8865668;
RA Mathews S., Sharrock R.A.;
RT "The phytochrome gene family in grasses (Poaceae): a phylogeny and
evidence that grasses have a subset of the loci found in dicot
angiosperms.";
RL Mol. Biol. Evol. 13:1141-1150(1996).
CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
```

NC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
XC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
XN NCBI_TaxID=3702;
XP [1]
XQ SEQUENCE FROM N.A.
XK STRAIN=cv. Columbia;
XX MEDLINE=20181125; PubMed=10718197;
YA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
IB Tabata S.;
IT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
IT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
IT clones.";
XK DNA Res. 7:31-63(2000).
XC -!- FUNCTION: INVOLVED IN TRANSPORT OF CATIONS (POTENTIAL).
XC -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
XC -!- SUBCELLULAR LOCATION: Integral membrane protein.
XC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
XC (E1-E2 ATPASES). SUBFAMILY V.
XC -----
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XC or send an email to license@isb-sib.ch).
XC -----
XK EMBL; AB025633; BAA97238.1; -
XR InterPro; IPR001757; ATPase_E1-E2.
XR InterPro; IPR001454; Hlgase/hydrilase.
XR Pfam; PF00122; E1-E2_ATPase; 1.
XR Pfam; PF00702; Hydrolase; 1.
XR PRINTS; PR00119; CATATPASE.
XR PROSITE; PS00154; ATPASE_E1_E2; 1.
XW Hydrolase; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
XW Magnesium.
XT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
TT TRANSMEM 21 42 POTENTIAL.
TT DOMAIN 43 50 EXTRACELLULAR (POTENTIAL).
TT TRANSMEM 51 71 POTENTIAL.
TT DOMAIN 72 192 CYTOPLASMIC (POTENTIAL).
TT TRANSMEM 193 215 POTENTIAL.
TT DOMAIN 216 218 EXTRACELLULAR (POTENTIAL).
TT TRANSMEM 219 238 POTENTIAL.
TT DOMAIN 239 402 CYTOPLASMIC (POTENTIAL).
TT TRANSMEM 403 422 POTENTIAL.
TT DOMAIN 423 435 EXTRACELLULAR (POTENTIAL).
TT TRANSMEM 436 453 POTENTIAL.
TT DOMAIN 454 947 CYTOPLASMIC (POTENTIAL).
TT TRANSMEM 948 967 POTENTIAL.
TT DOMAIN 968 979 EXTRACELLULAR (POTENTIAL).
TT TRANSMEM 980 997 POTENTIAL.
TT DOMAIN 998 1013 CYTOPLASMIC (POTENTIAL).
TT TRANSMEM 1014 1034 POTENTIAL.
TT DOMAIN 1035 1059 EXTRACELLULAR (POTENTIAL).
TT TRANSMEM 1060 1079 POTENTIAL.
TT DOMAIN 1080 1092 CYTOPLASMIC (POTENTIAL).
TT TRANSMEM 1093 1110 POTENTIAL.
TT DOMAIN 1111 1128 EXTRACELLULAR (POTENTIAL).
TT TRANSMEM 1129 1148 POTENTIAL.
TT DOMAIN 1149 1179 CYTOPLASMIC (POTENTIAL).
TT TRANSMEM 1175 1178 POLY-LYS.
TT MOD RES 491 491 PHOSPHORYLATION (BY SIMILARITY).
TT METAL 812 812 MAGNESIUM (BY SIMILARITY).
TT METAL 816 816 MAGNESIUM (BY SIMILARITY).
XQ SEQUENCE 1179 AA; 131115 MW; 4A3E82D222A4D78 CRC64;
Query Match 54.5%; Score 36; DB 1; Length 1179;
Best Local Similarity 44.4%; Pred.No. 56;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
NY 1 CFQWQKMR 9
|:|:|:

Db 1144 CYSWERLLR 1152

Search completed: February 21, 2003, 07:51:37
Job time : 6.2093 secs

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3M protein - protein search, using sw model

Run on: February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
(without alignments)
114.078 Million cell updates/sec

Title: US-09-743-107B-89

Perfect score: 66

Sequence: 1 CFQWQXMRKV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriapi:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	89.4	711	4 Q8TCD2	Q8Tcd2 homo sapien
2	55	83.3	38	4 Q9UCY5	Q9ucy5 homo sapien
3	50	75.8	33	6 Q9TR80	Q9tr80 ovis aries
4	41	62.1	105	10 Q9XFD5	Q9xfds oryza sativ
5	40	60.6	148	10 Q9XHP1	Q9xhp1 sesamum ind
6	40	60.6	275	5 Q93780	Q93780 caenorhabdi
7	40	60.6	932	5 Q19153	Q19153 caenorhabdi
8	39	59.1	205	16 Q986A0	Q986a0 rhizobium l
9	39	59.1	206	16 Q8UHC2	Q8unc2 agrobacteri
10	39	59.1	206	16 Q92RH8	Q92rh8 rhizobium m
11	39	59.1	208	16 Q8YFK3	Q8yfk3 brucella me
12	39	59.1	279	16 Q8XSE2	Q8xse2 ralstonia s
13	39	59.1	306	4 Q8TAX2	Q8tax2 homo sapien
14	39	59.1	466	4 Q9NUS2	Q9nus2 homo sapien
15	38	57.6	91	15 Q77855	Q77855 human immun
16	38	57.6	91	15 Q77856	Q77856 human immun

17	38	57.6	274	4 Q96W21	Q96w21 homo sapien
18	38	57.6	289	10 Q8C6N2	Q8c6n2 arabidopsis
19	38	57.6	515	10 Q218S5	Q218s5 arabidopsis
20	38	57.6	543	10 Q21889	Q21889 arabidopsis
21	38	57.6	1121	10 Q9SWS6	Q9sws6 lycopersico
22	37	56.1	85	16 Q8Z536	Q8z536 salmonella
23	37	56.1	109	15 Q9VQC1	Q9vqc1 human immun
24	37	56.1	109	15 Q9VQC0	Q9vqc0 human immun
25	37	56.1	109	15 Q9VQB9	Q9vqb9 human immun
26	37	56.1	109	15 Q9VQB8	Q9vqb8 human immun
27	37	56.1	109	15 Q9YJ17	Q9yj17 human immun
28	37	56.1	109	15 Q9YJ12	Q9yj12 human immun
29	37	56.1	115	15 Q9Q9L0	Q9q9l0 human immun
30	37	56.1	119	15 Q8Q454	Q8q454 human immun
31	37	56.1	121	16 Q8U6K3	Q8u6k3 agrobacteri
32	37	56.1	255	16 Q9A6E4	Q9a6e4 caulobacter
33	37	56.1	433	5 Q44473	Q44473 caenorhabdi
34	37	56.1	459	4 Q9NZW0	Q9nzw0 homo sapien
35	37	56.1	460	4 Q9NZW3	Q9nzw3 homo sapien
36	37	56.1	489	16 P96223	P96223 mycobacteri
37	37	56.1	509	10 Q9LHAI	Q9lhai arabidopsis
38	37	56.1	584	17 Q9HPA3	Q9hpa3 halobacteri
39	37	56.1	632	4 Q94937	Q94937 homo sapien
40	37	56.1	864	5 Q8Z582	Q8z582 encephalito
41	37	56.1	864	5 Q8SRG3	Q8srg3 encephalito
42	37	56.1	864	5 Q8SQ16	Q8sq16 encephalito
43	37	56.1	866	10 Q9FHI9	Q9fhi9 arabidopsis
44	36	54.5	377	12 Q91MQ5	Q91mq5 lumpy skin
45	36	54.5	393	10 Q9ZTP0	Q9ztp0 oryza sativ

ALIGNMENTS

RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.

AC Q8TCD2; TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347; AAH2347.1; -.
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7E097C45FAF CRC64;

Query Match 89.4%; Score 59; DB 4; Length 711;
Best Local Similarity 90.9%; Pred. No. 0.0067;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CFQWQXMRKV 11
|||||
Db 39 CFQWQXMRKV 49

RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.

AC Q9UCY5; TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE Lactoferrin homolog (Fragment).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RX MEDLINE=96081613; PubMed=8551695;
RA Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
RL Jpn. J. Legal Med. 49:281-293 (1995).
DR HSSP; P02788; 1BYA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDBEB CRC64;

Query Match 83.3%; Score 55; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWQXMRKVR 12
DB 21 FQWQXMRKVR 31

RESULT 3

Q9TR80 ID Q9TR80 PRELIMINARY; PRT; 33 AA.
AC Q9TR80;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]_SEQUENCE.
RP MEDLINE=95127729; PubMed=7827104;
RX Qian Z.Y., Jolles P., Migliore-Samouri D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32 (1995).
DR HSSP; O77698; 1CE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAB15A73961 CRC64;

Query Match 75.8%; Score 50; DB 6; Length 33;
Best Local Similarity 63.6%; Pred. No. 0.014;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQXMRKV 11
DB 19 CFQWQXMRKV 29

RESULT 4

Q9XFD5 ID Q9XFD5 PRELIMINARY; PRT; 105 AA.
AC Q9XFD5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]_SEQUENCE FROM N.A.
RP TISSUE=PANICLE;
RA Liu J., Yang J.;
RT "Suppression subtractive hybridization (SSH) identified candidate

RT genes that are differentially expressed at rice young panicle.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC [1]_SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF140486; AAS29899.1; --
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON TER 1
SQ SEQUENCE 105 AA; 11912 MW; B0E8FCD487E19F9 CRC64;

Query Match 62.1%; Score 41; DB 10; Length 105;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQXMRK 10
DB 61 CFQWQXMRK 70

RESULT 5

Q9XHP1 ID Q9XHP1 PRELIMINARY; PRT; 148 AA.
AC Q9XHP1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]_SEQUENCE FROM N.A.
RP STRAIN=TAINAN 1;
RX MEDLINE=20074970; PubMed=10606554;
RA Tai S.S.K., Wu L.S.H., Chen E.C.P., Tzen J.T.C.;
RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed
RT storage proteins in sesame.";
RL J. Agric. Food Chem. 47:4932-4938 (1999).
DR EMBL; AF091841; AAD42943.1; --
DR InterPro; IPR003612; AAI.
DR InterPro; IPR000617; Napin.
DR InterPro; IPR001768; Try/amyL_inhbr.
DR Pfam; PF00234; tryp_alpha_ami1; 1.
DR PRINTS; PR00496; NAPIN.
DR SMART; SMO0499; AAI; 1.
SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 60.6%; Score 40; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQXMRK 9
DB 54 CFQWQXMRK 62

RESULT 6

Q93780 ID Q93780 PRELIMINARY; PRT; 275 AA.
AC Q93780;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F53H4.4 protein.
GN F53H4.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

N
P
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Q

[1]
SEQUENCE FROM N.A.
Dobson R.; Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
none;
"Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
ENBL; Z81089; CAB03137.1; -.
Q SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 60.6%; Score 40; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 9.7;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Y 2 FQWQXMRKVR 12
|||: |||
b 262 FQWKISMRKTR 272

RESULT 7
19153
D Q19153 PRELIMINARY; PRT; 932 AA.
T Q19153;
T 01-NOV-1996 (TrEMBLrel. 01, Created)
T 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
T 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
E Hypothetical 105.1 kDa protein.
N F07C3.1.
S Caenorhabditis elegans.
C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
C Rhabditidae; Peloderinae; Caenorhabditis.
X NCBI_TaxID=6239;

N [1]
P SEQUENCE FROM N.A.
C STRAIN=BRISTOL N2;
C MEDLINE=99069613; PubMed=9851916;
A None;
T "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
[2]
P SEQUENCE FROM N.A.
C STRAIN=BRISTOL N2;
C STRAIN=BRISTOL N2;
C STRAIN=BRISTOL N2;
C STRAIN=BRISTOL N2;
A Waterston R.;
T "Direct Submission.";
L Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
R ENBL; U50308; AAG24025.1; -.
R InterPro; IPR000731; HMGC/patch_5TM.
R PROSITE; PS50156; SSD; 1.
W Hypothetical protein.
Q SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;

Query Match 60.6%; Score 40; DB 5; Length 932;
Best Local Similarity 63.6%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Y 2 FQWQXMRKVR 12
|||: |||
b 579 FQWQSRARLVK 589

RESULT 8
986A0

ID Q986A0 PRELIMINARY; PRT; 205 AA.
AC Q986A0;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Pyridoxamine 5'-phosphate oxidase.
GN MLL7454.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=VAFE303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Watanabe A., Ideasa Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Kaneko T., Nakamura K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP03011; BAB5353.1; -.
DR InterPro; IPR000659; Pyridox_oxidase.
DR Pfam; PF01243; Pyridox_oxidase; 1.
DR ProDom; PD006312; Pyridox_oxidase; 1.
DR TIGRFAMs; TIGR00558; pdxH; 1.
DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
KW Complete proteome.
SQ SEQUENCE 205 AA; 23300 MW; 0BADE4CD12327EA CRC64;

Query Match 59.1%; Score 39; DB 16; Length 205;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
|||: |||
Db 88 CFHWKSLRRQVR 99

RESULT 9
Q8UHC2 PRELIMINARY; PRT; 206 AA.
ID Q8UHC2;
AC Q8UHC2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Pyridoxamine 5'-phosphate oxidase.
GN PDXH OR ATU0760 OR AGR_C1381.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayvin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;

RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houtiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58";
 RL Science 294:2323-2328(2001).
 DR ENBL; AB009043; AAL41776.1; -;
 DR ENBL; AB008009; AAK86569.1; -;
 KW Complete proteome.
 SQ SEQUENCE 206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;

Query Match 59.1%; Score 39; DB 16; Length 206;

Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
 ||| | | | | | | |
 Db 88 CFHWKSLRRQVR 99

RESULT 10

Q92RH8 ID Q92RH8 PRELIMINARY; PRT; 206 AA.
 AC Q92RH8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
 DE (EC 1.4.3.5).
 GN PDHX OR R00895 OR SMC00069.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capella D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godrie T., Coffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetelle D., Puhler A., Purnelle B., Rampsberger U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR ENBL; AL591785; CAC45467.1; -;
 DR InterPro; IPR000659; Pyridox_oxidase.
 DR Pfam; PF01243; Pyridox_oxidase; 1.
 DR ProDom; PD006312; Pyridox_oxidase; 1.
 DR TIGRFAMs; TIGR00558; pdxH; 1.
 DR PROSITE; PS01064; PYRIDOX_OXIDASE; UNKNOWN_1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 206 AA; 23900 MW; A2D874229DACA97A CRC64;

Query Match 59.1%; Score 39; DB 16; Length 206;

Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
 ||| | | | | | | |
 Db 88 CFHWKSLRRQVR 99

RESULT 11

Q8YFK3 ID Q8YFK3 PRELIMINARY; PRT; 208 AA.
 AC Q8YFK3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5).
 GN BME11517.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
 RA Ivanova N., Anderson I., Shattacharyya A., Lykidis A., Reznik G.,
 RA Jablonki L., Larsen N., D'Souza M., Bernal A., Mazur M., Coleman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kypides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009587; AAL52698.1; -;
 DR InterPro; IPR000659; Pyridox_oxidase.
 DR Pfam; PF01243; Pyridox_oxidase; 1.
 DR ProDom; PD006312; Pyridox_oxidase; 1.
 DR TIGRFAMs; TIGR00558; pdxH; 1.
 DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
 KW Oxidoreductase; Complete Proteome.
 SQ SEQUENCE 208 AA; 23866 MW; CB1F50BC9612DE28 CRC64;

Query Match 59.1%; Score 39; DB 16; Length 208;

Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
 ||| | | | | | | |
 Db 90 CFHWKSLRRQVR 101

RESULT 12

Q8XSE2 ID Q8XSE2 PRELIMINARY; PRT; 279 AA.
 AC Q8XSE2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative ICC protein homolog.
 DE ICC OR RSP0534 OR RS00414.
 GN Ralstonia solanacearum (Pseudomonas solanacearum).
 OS Ralstonia solanacearum.
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646079; CAD17685.1; -;
 DR InterPro; IPR004843; M-Ppstrase.
 DR InterPro; IPR004844; S/T_phosphatase.
 DR Pfam; PF00149; Metallophos; 1.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 279 AA; 31541 MW; ABB38818004B2EDA CRC64;

Query Match 59.1%; Score 39; DB 16; Length 279;

Best Local Similarity 41.7%; Pred. No. 15;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Y 1 CFQWQXMRKVR 12
  ||||:|
b 244 CFQWKGRTAK 255

RESULT 13
18TAX2
D Q8TAX2 PRELIMINARY; PRT; 306 AA.
C Q8TAX2;
T 01-JUN-2002 (TEMBLrel. 21, Created)
T 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
T 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
E Similar to hypothetical protein FL011175.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
M Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
P SEQUENCE FROM N.A.
C TISSUE=PANCREAS;
A Strausberg R.;
L Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
R EMBL; BC025708; AAH25708.1; -.
W Hypothetical protein.
Q SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;

Query Match 59.1%; Score 39; DB 4; Length 306;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Y 1 CFQWQXMR 9
  ||||:|
b 269 CFQWESTLR 277

RESULT 14
19NUS2
D Q9NUS2 PRELIMINARY; PRT; 466 AA.
C Q9NUS2;
T 01-OCT-2000 (TEMBLrel. 15, Created)
T 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
T 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
E CDNA FLJ11175 fis, clone PLACE1007375, weakly similar to phorbol
  ester/diacylglycerol-binding protein UNC-13.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
M Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
P SEQUENCE FROM N.A.
C TISSUE=PLACENTA;
A Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
  A Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
  A Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
  A Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
  A Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
  A Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
  A Ninomiya K., Iwayanagi T.;
T "NEDO human cDNA sequencing project.";
L Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
R EMBL; AK020377; BAA92048.1; -.
R HSSP; P21707; IBYN.
R InterPro; IPR000008; C2.
R InterPro; IPR000504; RNA_rec_mot.
R Pfam; PF00168; C2; 1.
R PRINTS; PR00160; C2DOWN.
R SMART; SM0239; C2; 1.
R PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
R PROSITE; PS00004; C2_DOMAIN_2; 1.
R PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
Q SEQUENCE 466 AA; 53192 MW; E4113A5062F58D6E CRC64;
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Query Match 59.1%; Score 39; DB 4; Length 466;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQXMR 9
  ||||:|
Db 269 CFQWESTLR 277

RESULT 15
Q77855 PRELIMINARY; PRT; 91 AA.
AC Q77855;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Envelope protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95191002; PubMed=7884875;
RA Mulder-Kampinea G.A., Simonon A., Kuiken C.L., Dekker J.,
  RA Scherpbier H.J., de Perre P., Boer K., Goudamit J.;
RT "Similarity in env and gag genes between genomic RNAs of human
  RT immunodeficiency virus type 1 (HIV-1) from mother and infant is
  RL J. Virol. 69:2285-2296(1995).
DR EMBL; Z47867; CAA87881.1; -.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT TER 91
SQ SEQUENCE 91 AA; 10530 MW; 8B10C62011F305D6 CRC64;

Query Match 57.6%; Score 38; DB 15; Length 91;
Best Local Similarity 60.0%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWQXMRKVR 12
  ||||:|
Db 67 QWNRTLQKVR 76

Search completed: February 21, 2003, 08:00:43
Job time: 21.6744 secs
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DM protein - protein search, using sw model

Run on: February 21, 2003, 07:37:21 / Search time 28.093 Seconds
(without alignments)
56.918 Million cell updates/sec

Title: US-09-743-107b-90

Perfect score: 66

Sequence: 1 CFQQRXKVR 12

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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A Geneseq_101002.*

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- 7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	98.5	12	21	AA1980.DAT.*
2	64	97.0	12	21	AA1981.DAT.*
3	64	97.0	12	21	AA1982.DAT.*
4	64	97.0	12	21	AA1983.DAT.*
5	64	97.0	12	21	AA1984.DAT.*
6	64	97.0	12	21	AA1985.DAT.*
7	64	97.0	12	21	AA1986.DAT.*
8	64	97.0	12	21	AA1987.DAT.*
9	64	97.0	12	21	AA1988.DAT.*
10	64	97.0	12	21	AA1989.DAT.*

11	64	97.0	14	21	AA198036	Human lactoferrin
12	64	97.0	14	21	AA198050	Human lactoferrin
13	64	97.0	14	21	AA198051	Human lactoferrin
14	64	97.0	15	17	AA198054	Peptide for anti-u
15	64	97.0	15	21	AA198035	Human lactoferrin
16	64	97.0	15	21	AA198062	Human lactoferrin
17	64	97.0	15	21	AA198063	Human lactoferrin
18	64	97.0	16	21	AA198031	Human lactoferrin
19	64	97.0	16	21	AA198064	Human lactoferrin
20	64	97.0	16	21	AA198065	Human lactoferrin
21	64	97.0	17	21	AA198034	Human lactoferrin
22	64	97.0	17	21	AA198066	Human lactoferrin
23	64	97.0	17	21	AA198067	Human lactoferrin
24	64	97.0	18	15	AA198352	Advanced glycosyla
25	64	97.0	18	17	AA198397	Human lactoferrin
26	64	97.0	18	21	AA198033	Human lactoferrin
27	64	97.0	19	21	AA198867	Amino acid sequenc
28	64	97.0	19	21	AA198032	Human lactoferrin
29	64	97.0	20	13	AA19821810	Anti microbial pep
30	64	97.0	20	14	AA1984841	Lactoferrin-relate
31	64	97.0	20	15	AA1984530	Lactoferrin derive
32	64	97.0	20	15	AA198531	Lactoferrin derive
33	64	97.0	20	15	AA1987461	Lactoferrin derive
34	64	97.0	20	15	AA1987462	Lactoferrin derive
35	64	97.0	20	16	AA1984698	Bovine lactoferrin
36	64	97.0	20	16	AA1984599	Bovine lactoferrin
37	64	97.0	20	16	AA1980263	Anti-parasitic lac
38	64	97.0	20	16	AA1980264	Anti-parasitic lac
39	64	97.0	20	17	AA198553	Peptide for anti-u
40	64	97.0	20	17	AA1981852	Lactoferrin-derive
41	64	97.0	20	17	AA1980345	Lactoferrin-derive
42	64	97.0	20	17	AA1980607	Lactoferrin-derive
43	64	97.0	20	17	AA1987821	Lactoferrin-derive
44	64	97.0	20	17	AA1987822	Lactoferrin-derive
45	64	97.0	20	18	AA19826150	Lactoferrin deriva

ALIGNMENTS

RESULT 1

AA198074

ID AA198074 standard; Peptide; 12 AA.

AC AA198074;

DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:74.

Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.

OS Homo sapiens.

OS Synthetic.

PN WO200001730-A1.

PD 13-JAN-2000.

PF 06-JUL-1999; 99WO-S601230.

PR 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

PA (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer I, Dolphin GT;

XX WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections, -
 XX PT inflammations and tumors and for use in infant formula food -
 XX PS Claim 22; Page 35; 102pp; English.
 XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides can also be used
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX CC
 SQ Sequence 12 AA;
 Query Match 98.5%; Score 65; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 5.3e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRXMRKVR 12
 DB 1 CFQWQRXMRKVR 12
 RESULT 2
 AAY78038
 ID AAY78038 standard; Peptide; 12 AA.
 AC AAY78038;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:38.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 EN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections, -
 XX PT inflammations and tumors and for use in infant formula food -
 XX PS Claim 12; Page 70; 102pp; English.
 XX CC AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX CC
 SQ Sequence 12 AA;
 Query Match 97.0%; Score 64; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 7.9e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRXMRKVR 12
 DB 1 CFQWQRXMRKVR 12
 RESULT 3
 AAY78046
 ID AAY78046 standard; Peptide; 12 AA.
 AC AAY78046;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:46.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 EN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections, -
 XX PT inflammations and tumors and for use in infant formula food -
 XX PS Claim 15; Page 35; 102pp; English.
 XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also

C fungicidal and bactericidal and may also be used as preservatives.
C Even though native human lactoferrin have been shown to have desired
C anti-inflammatory anti-infectious and anti-tumoural properties they
C cannot be used clinically on a broad basis because of high production
C costs. Therefore, provision of peptides based on lactoferrin would
C enable them to be used for the same purposes as lactoferrin at lower
C cost.

Q Sequence 12 AA;

Query Match 97.0%; Score 64; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQWQRMKVR 12
b 1 CFQWQRMKVR 12

RESULT 4

AY78047
D AAY78047 standard; Peptide; 12 AA.

C AAY78047;

X 25-APR-2000 (first entry)

X Human lactoferrin derived peptide SEQ ID NO:47.

X Human; lactoferrin; modification; infection; inflammation; tumour;
X food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
X urinary tract infection; colitis; Candida infection; fungicidal;
X bactericidal; preservative.

X Homo sapiens.

X Synthetic.

X WO200001730-A1.

X 13-JAN-2000.

X 06-JUL-1999; 99WO-SB01230.

X 06-JUL-1998; 98SE-0002441.

X 17-JUL-1998; 98SE-0002562.

X 29-DEC-1998; 98SE-0004614.

X (ASCI-) A+ SCI INVEST AB.

X Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

X WPI; 2000-147388/13.
X New peptides used for treatment and prevention of infections,
X inflammations and tumors and for use in infant formula food -

X Claim 18; Page 73; 102pp; English.

X AAY78001 to AAY78100 represent peptides having sequences based on human
X lactoferrin. The peptides are taken up in the intestine through
X binding to specific lactoferrin receptors and are then transported
X through the circulation. A medicinal product of the peptide or fragment
X can be used for treating and/or prevention of infections (such as
X urinary tract infections, colitis, and Candida infection on a mucosal
X membrane), inflammations and/or tumors. The peptides can also be used
X in food stuffs such as infant formula food. The peptides are also
X fungicidal and bactericidal and may also be used as preservatives.
X Even though native human lactoferrin have been shown to have desired
X anti-inflammatory anti-infectious and anti-tumoural properties they
X cannot be used clinically on a broad basis because of high production
X costs. Therefore, provision of peptides based on lactoferrin would
X enable them to be used for the same purposes as lactoferrin at lower
X cost.

XX Sequence 12 AA;

Query Match 97.0%; Score 64; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
Db 1 CFQWQRMKVR 12

RESULT 5

AY78086
ID AAY78086 standard; Peptide; 12 AA.

XX AAY78086;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:86.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SB01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
XX inflammations and tumors and for use in infant formula food -

XX Claim 22; Page 36; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
XX lactoferrin. The peptides are taken up in the intestine through
XX binding to specific lactoferrin receptors and are then transported
XX through the circulation. A medicinal product of the peptide or fragment
XX can be used for treating and/or prevention of infections (such as
XX urinary tract infections, colitis, and Candida infection on a mucosal
XX membrane), inflammations and/or tumors. The peptides can also be used
XX in food stuffs such as infant formula food. The peptides are also
XX fungicidal and bactericidal and may also be used as preservatives.
XX Even though native human lactoferrin have been shown to have desired
XX anti-inflammatory anti-infectious and anti-tumoural properties they
XX cannot be used clinically on a broad basis because of high production
XX costs. Therefore, provision of peptides based on lactoferrin would
XX enable them to be used for the same purposes as lactoferrin at lower
XX cost.

XX Sequence 12 AA;

Query Match 97.0%; Score 64; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
 Db 1 CFQWQXMRKVR 12

RESULT 6

ID AAY78089 standard; Peptide; 12 AA.

XX AAY78089;
 XX 25-APR-2000 (first entry)
 DE Human lactoferrin derived peptide SEQ ID NO:89.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 22; Page 37; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;

Query Match 97.0%; Score 64; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.9e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
 Db 1 CFQWQXMRKVR 12

RESULT 7

AAY78090

ID AAY78090 standard; Peptide; 12 AA.

XX AAY78090;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:90.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 22; Page 37; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;

Query Match 97.0%; Score 64; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.9e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
 Db 1 CFQWQXMRKVR 12

RESULT 8

AAY78037

ID AAY78037 standard; Peptide; 13 AA.

XX AAY78037;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200001730-A1.
 XX 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 12; Page 70; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 13 AA;
 Query Match 97.0%; Score 64; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 8.6e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 2Y 1 CFQWQRXMRKVR 12
 |||||
 Db 2 CFQWQRNMRKVR 13
 RESULT 9
 AAY78048
 ID AAY78048 standard; Peptide; 13 AA.
 XX
 AC AAY78048;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:48.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.

OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 15; Page 74; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 13 AA;
 Query Match 97.0%; Score 64; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 8.6e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 2Y 1 CFQWQRXMRKVR 12
 |||||
 Db 2 CFQWQRNMRKVR 13
 RESULT 10
 AAY78049
 ID AAY78049 standard; Peptide; 13 AA.
 XX
 AC AAY78049;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:49.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 XX Claim 18; Page 74; 102pp; English.
 PS
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 97.0%; Score 64; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 8.6e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRMKVR 12
 DB 2 CFQWQRMKVR 13
 RESULT 11
 AAY78036
 ID AAY78036 standard; Peptide; 14 AA.
 XX
 AC AAY78036;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:36.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200001730-A1.
 PD 13-JAN-2000.
 XX
 PP 06-JUL-1999; 99WO-SE01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 XX Claim 12; Page 69; 102pp; English.
 PS
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 97.0%; Score 64; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 9.2e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRMKVR 12
 DB 3 CFQWQRMKVR 14
 RESULT 12
 AAY78050
 ID AAY78050 standard; Peptide; 14 AA.
 XX
 AC AAY78050;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:50.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200001730-A1.
 PD 13-JAN-2000.
 XX
 PP 06-JUL-1999; 99WO-SE01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX

PS Claim 15; Page 75; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infections and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 14 AA;

Query Match 97.0%; Score 64; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 9.2e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQWQXMRKVR 12
 |||||
 b 3 CFQWQXMRKVR 14

RESULT 13

AY78051
 D AAY78051 standard; Peptide; 14 AA.

AY78051;

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:51.

Human; lactoferrin; modification; infection; inflammation; tumour;
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 urinary tract infection; colitis; Candida infection; fungicidal;
 bactericidal; preservative.

Homo sapiens.
 Synthetic.

WO200001730-A1.

13-JAN-2000.

06-JUL-1999; 99WO-S01230.

06-JUL-1998; 98SE-0002441.

17-JUL-1998; 98SE-0002562.

29-DEC-1998; 98SE-0004614.

(ASCII-) A+ SCI INVEST AB.

Hanson LA, Matsby-Baltzer I, Baltzer L, Dolphin GT;

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections, -

inflammations and tumors and for use in infant formula food

Claim 18; Page 75; 102pp; English.

AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infections and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 14 AA;

Query Match 97.0%; Score 64; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 9.2e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQWQXMRKVR 12
 |||||
 b 3 CFQWQXMRKVR 14

RESULT 14

AY78554
 ID AAR98554 standard; Peptide; 15 AA.

AY78554;

12-NOV-1996 (first entry)

Peptide for anti-ulcer agent.

anti-ulcer agent; low toxicity; stable; heat-resistant.

Synthetic.

JP08143468-A.

04-JUN-1996.

17-NOV-1994; 94JP-0283869.

17-NOV-1994; 94JP-0283869.

(MORG) MORINAGA MILK IND CO LTD.

WPI; 1996-318857/32.

Anti-ulcer agent contg. peptide - has low toxicity, is
 heat-resistant and water-soluble

Claim 1; Page 11; 11pp; Japanese.

AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
 CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
 CC administered orally and be produced in large amounts.

XX Sequence 15 AA;

Query Match 97.0%; Score 64; DB 17; Length 15;
 Best Local Similarity 91.7%; Pred. No. 9.8e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQWQXMRKVR 12
 |||||
 b 2 CFQWQXMRKVR 13

RESULT 15

AY78035
 ID AAY78035 standard; Peptide; 15 AA.

AY78035;

XX 25-APR-2000 (first entry)
DT Human lactoferrin derived peptide SEQ ID NO:35.
XX
DE Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections, -
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 12; Page 69; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 15 AA;
Query Match 97.0%; Score 64; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 9.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWQRXNRKVR 12
Db 4 CFQWQRXNRKVR 15

Search completed: February 21, 2003, 07:56:43
Job time : 28.093 secs

GenCore version 5.1.3
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DM protein - protein search, using sw model

Run on: February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds
(without alignments)
39.537 Million cell updates/sec

Title: US-09-743-107B-90

Perfect score: 66

Sequence: 1 CFQWQRMRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

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6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	64	97.0	18	1	US-08-204-487-3
2	64	97.0	18	2	US-08-485-948-8
3	64	97.0	18	2	US-08-628-380-8
4	64	97.0	18	2	US-08-475-055-8
5	64	97.0	20	1	US-07-755-161A-3
6	64	97.0	20	1	US-07-891-174-3
7	64	97.0	20	1	US-08-204-487-1
8	64	97.0	20	1	US-08-256-771-24
9	64	97.0	20	1	US-08-256-771-25
10	64	97.0	20	1	US-08-381-984-24
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12	64	97.0	22	4	US-09-508-734-4
13	64	97.0	22	4	US-09-508-734-6
14	64	97.0	25	1	US-07-755-161A-10
15	64	97.0	25	1	US-07-891-174-10
16	64	97.0	25	1	US-08-204-487-7
17	64	97.0	29	4	US-09-508-734-8
18	64	97.0	36	1	US-07-755-161A-8
19	64	97.0	36	1	US-07-891-174-8
20	64	97.0	36	1	US-08-256-771-30
21	64	97.0	36	1	US-08-381-984-29
22	64	97.0	47	2	US-08-464-182A-6
23	64	97.0	47	2	US-08-406-271-6
24	64	97.0	50	2	US-08-693-274A-7
25	64	97.0	52	4	US-09-017-043A-3
26	64	97.0	53	2	US-08-464-182A-5
27	64	97.0	53	2	US-08-406-271-5

28	64	97.0	54	2	US-08-464-182A-2	Sequence 2, Appli
29	64	97.0	54	2	US-08-406-271-2	Sequence 2, Appli
30	64	97.0	694	3	US-08-724-586-2	Sequence 2, Appli
31	64	97.0	694	4	US-09-421-632-2	Sequence 2, Appli
32	64	97.0	694	4	US-09-932-190-2	Sequence 2, Appli
33	64	97.0	705	2	US-08-655-640-2	Sequence 2, Appli
34	64	97.0	708	2	US-08-655-640-4	Sequence 4, Appli
35	64	97.0	711	1	US-08-354-019-4	Sequence 4, Appli
36	64	97.0	711	1	US-08-461-333-4	Sequence 4, Appli
37	64	97.0	711	3	US-08-464-167-4	Sequence 4, Appli
38	64	97.0	711	3	US-09-158-313-4	Sequence 4, Appli
39	64	97.0	711	4	US-08-476-798-4	Sequence 4, Appli
40	61	92.4	711	1	US-08-145-681-2	Sequence 2, Appli
41	61	92.4	711	1	US-08-250-308-2	Sequence 2, Appli
42	61	92.4	711	1	US-08-453-703-2	Sequence 2, Appli
43	61	92.4	711	2	US-08-456-106-2	Sequence 2, Appli
44	61	92.4	711	3	US-08-456-108-2	Sequence 2, Appli
45	61	92.4	711	4	US-09-265-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32, 503
; REFERENCE/DOCKET NUMBER: FUN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 97.0%; Score 64; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKVR 12
Db 1 CFQWQRMKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 585582
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-485-948-8

Query Match 97.0%; Score 64; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKVR 12
Db 1 CFQWQRMKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-628-380-8

Query Match 97.0%; Score 64; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 3.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMKVR 12
Db 1 CFQWQRMKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match 97.0%; Score 64; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 3,8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2Y 1 CFQWQRMKVR 12
   |||||
3B 1 CFQWQRMKVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KB
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
* RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
Query Match 97.0%; Score 64; DB 1; Length 20;
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Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRXMRKVR 12
Db 2 CFQWRXMRKVR 13

RESULT 6
US-07-891-174-3
Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRXMRKVR 12
Db 2 CFQWRXMRKVR 13

RESULT 7
US-08-204-487-1
Sequence 1, Application US/08204487
Patent No. 5585425
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHITIRO
APPLICANT: UCHIDA, TOSHIKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOPERRIN"
US-08-204-487-1

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWRXMRKVR 12
b 2 CFQWRXMRKVR 13

RESULT 8
US-08-256-771-24
Sequence 24, Application US/08256771
Patent No. 5658591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWRXMRKVR 12
Db 2 CFQWRXMRKVR 13

RESULT 9
US-08-256-771-25
Sequence 25, Application US/08256771
Patent No. 5658591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWRXMRKVR 12
Db 2 CFQWRXMRKVR 13

RESULT 10
US-08-381-984-24

Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "the specified peptide as well as

OTHER INFORMATION: peptides including the specified peptide as a fragment thereof

US-08-381-984-24

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12

DB 2 CFQWQRMKVR 13

RESULT 11

US-08-381-984-25
Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "the specified peptide as well as

OTHER INFORMATION: peptides including the specified peptide as a fragment thereof

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "cysteine residues at positions 2

OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"

US-08-381-984-25

Query Match 97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12

DB 2 CFQWQRMKVR 13

RESULT 12

US-09-508-734-4
Sequence 4, Application US/09508734
Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Sanyang Genex Corporation

TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
FILE REFERENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: PCT/KE99/00373

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: KR1998-29351

PRIOR FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4

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; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
JS-09-508-734-4

Query Match          97.0%; Score 64; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 4.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2y 1 CFQWQRNMRKVR 12
   |||||
2b 2 CFQWQRNMRKVR 13

RESULT 13
JS-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
JS-09-508-734-6

Query Match          97.0%; Score 64; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2y 1 CFQWQRNMRKVR 12
   |||||
2b 3 CFQWQRNMRKVR 14

RESULT 14
JS-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-755-161A-10

Query Match          97.0%; Score 64; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 5.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRNMRKVR 12
   |||||
Db 4 CFQWQRNMRKVR 15
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RESULT 15
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21

; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-891-174-10
; Query Match 97.0%; Score 64; DB 1; Length 25;
; Best Local Similarity 91.7%; Pred. No. 5.2e-05;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; QY 1 CFQWQRXMRKVR 12
; Db 4 CFQWQRXMRKVR 15
; Search completed: February 21, 2003, 08:04:26
; Job time : 8.93023 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 08:08:15 ; Search time 6.88372 Seconds
(without alignments)
54.162 Million cell updates/sec

Title: US-09-743-107b-90

Perfect score: 66

Sequence: 1 CFQWRXMRKVR 12

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Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	64	97.0	25	9	US-09-798-869-20
3	64	97.0	694	9	US-10-023-096-2
4	56	84.8	15	9	US-09-798-869-6
5	53	80.3	15	9	US-09-798-869-3
6	53	80.3	25	9	US-09-798-869-23
7	45	68.2	15	9	US-09-798-869-7
8	44	66.7	15	9	US-09-798-869-4
9	44	66.7	25	9	US-09-798-869-22
10	41	62.1	15	9	US-09-798-869-8
11	41	62.1	15	9	US-09-798-869-29
12	41	62.1	15	9	US-09-798-869-30
13	37	56.1	21	10	US-09-864-761-47985
14	37	56.1	489	9	US-09-888-320-2
15	36	54.5	209	10	US-09-904-536-8
16	36	54.5	209	10	US-09-904-536-9
17	36	54.5	209	10	US-09-904-536-11
18	36	54.5	209	10	US-09-904-536-12
19	36	54.5	209	10	US-09-904-536-13

20	36	54.5	209	10	US-09-904-536-14	Sequence 14, Appl
21	36	54.5	209	10	US-09-904-536-15	Sequence 15, Appl
22	36	54.5	209	10	US-09-904-536-16	Sequence 16, Appl
23	36	54.5	209	10	US-09-904-536-17	Sequence 17, Appl
24	36	54.5	209	10	US-09-904-536-18	Sequence 18, Appl
25	36	54.5	212	10	US-09-904-536-10	Sequence 10, Appl
26	36	54.5	235	9	US-10-095-449-6	Sequence 6, Appl
27	36	54.5	235	10	US-09-448-378-1	Sequence 1, Appl
28	36	54.5	235	10	US-09-983-806-6	Sequence 6, Appl
29	36	54.5	235	10	US-09-904-536-1	Sequence 1, Appl
30	35	53.0	86	9	US-09-738-626-5715	Sequence 5715, Ap
31	34	51.5	95	10	US-09-764-864-1031	Sequence 1031, Ap
32	34	51.5	846	9	US-10-051-409-4	Sequence 4, Appl
33	34	51.5	1617	9	US-10-090-453A-2	Sequence 2, Appl
34	33	50.0	15	9	US-09-798-869-5	Sequence 5, Appl
35	33	50.0	46	10	US-09-864-761-48879	Sequence 48879, A
36	33	50.0	579	10	US-09-824-588-2	Sequence 2, Appl
37	32.5	49.2	124	10	US-09-864-761-44327	Sequence 44327, A
38	32	48.5	13	9	US-09-798-869-26	Sequence 26, Appl
39	32	48.5	14	9	US-09-798-869-25	Sequence 25, Appl
40	32	48.5	15	9	US-09-798-869-1	Sequence 1, Appl
41	32	48.5	15	9	US-09-798-869-10	Sequence 10, Appl
42	32	48.5	15	9	US-09-798-869-28	Sequence 28, Appl
43	32	48.5	18	9	US-09-798-869-24	Sequence 24, Appl
44	32	48.5	25	9	US-09-798-869-21	Sequence 21, Appl
45	32	48.5	25	10	US-09-909-652-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 97.0%; Score 64; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 2.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWRXMRKVR 12

DB 3 CFQWRXMRKVR 14

RESULT 2

US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON

APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match 97.0%; Score 64; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRXMRKVR 12
| | | | | | | | | |
Db 3 CFQWRXMRKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kureski, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-10-023-096-2

Query Match 97.0%; Score 64; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.00096;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWRXMRKVR 12
| | | | | | | | | |
Db 22 CFQWRXMRKVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON)
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match 84.8%; Score 56; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.00062;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWRXMRKVR 12
| | | | | | | | | |
Db 3 CFQWRXMRKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON)
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

Query Match 80.3%; Score 53; DB 9; Length 15;
Best Local Similarity 72.7%; Pred. No. 0.0021;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQWQRMKRV 11
|:|||||
b 3 CYQWQRMKRL 13

RESULT 6
US-09-798-869-23
Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 25
TYPE: PRT
ORGANISM: CAPRINE
US-09-798-869-23

Query Match 80.3%; Score 53; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 0.0034;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQWQRMKRV 11
|:|||||
b 3 CYQWQRMKRL 13

RESULT 7
US-09-798-869-7
Sequence 7, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
OTHER INFORMATION: sequence)

Query Match 68.2%; Score 45; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.051;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

US-09-798-869-7

Y 1 CFQWQRMKRV 11
|:|||||
b 3 CYQWQRMKRL 13

RESULT 8
US-09-798-869-4
Sequence 4, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 15
TYPE: PRT
ORGANISM: MURINE
US-09-798-869-4

Query Match 66.7%; Score 44; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.077;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Y 1 CFQWQRMKRV 11
|:|||||
b 3 CLRQWQRMKRV 13

RESULT 9
US-09-798-869-22
Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 25
TYPE: PRT
ORGANISM: MURINE
US-09-798-869-22

Query Match 66.7%; Score 44; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.12;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Y 1 CFQWQRMKRV 11
|:|||||
b 3 CLRQWQRMKRV 13

RESULT 10
US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8

Query Match 62.1%; Score 41; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.26;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11
|:|:|:|:|:
Db 3 CLRWQEMKVL 13

RESULT 11
US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 62.1%; Score 41; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.26;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11
|:|:|:|:|:
Db 3 CLRWQEMKVL 13

RESULT 12
US-09-798-869-30

; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ(RNSSON
; APPLICANT: LARS VORLAND
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30

Query Match 62.1%; Score 41; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.26;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKRV 11
|:|:|:|:|:
Db 3 CLRWQEMKVL 13

RESULT 13
US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,697
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 47985
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL096701.14
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
;; OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUATE 1.00e-06

IS-09-864-761-47985

Query Match 56.1%; Score 37; DB 10; Length 21;
Best Local Similarity 53.3%; Pred. No. 1.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CFQWOR 6
|||:
b 16 CFQWR 21

RESULT 14

IS-09-888-320-2
Sequence 2, Application US/09888320
Publication No. US20030013090A1
GENERAL INFORMATION:
APPLICANT: Barry III, Clifton E.
APPLICANT: DeBarber, Andrea E.
APPLICANT: Mduliri, Khisimuzi
APPLICANT: Bekker, Linda-Gail
APPLICANT: The Government of the United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REFERENCE: 015280-413100US
CURRENT APPLICATION NUMBER: US/09/888,320
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 2
LENGTH: 489
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
IS-09-888-320-2

Query Match 56.1%; Score 37; DB 9; Length 489;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Y 1 CFQWORXMRKV 11
|||:
b 253 CQKWRFRMRKM 263

RESULT 15

IS-09-904-536-8
Sequence 8, Application US/09904536
Patent No. US20020111475A1
GENERAL INFORMATION:

;; APPLICANT: Graddis, Thomas J.
;; APPLICANT: McGrew, Jeffrey T.
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
;; FILE REFERENCE: 03260.0028
;; CURRENT APPLICATION NUMBER: US/09/904,536
;; CURRENT FILING DATE: 2001-07-16
;; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
;; PRIOR FILING DATE: 1999-07-02
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn ver. 2.1
;; SEQ ID NO 8
;; LENGTH: 209
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-09-904-536-8

Query Match 54.5%; Score 36; DB 10; Length 209;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWORXMRK 10
|||:
Db 178 CLHWQRTTTR 187

Search completed: February 21, 2003, 08:11:56
Job time : 7.88372 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:48:01 ; Search time 10.6047 Seconds
(without alignments)
108.784 Million cell updates/sec

Title: US-09-743-107b-90

Perfect score: 66

Sequence: 1 CFQWQXMKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	97.0	711	1 TFHUL	lactotransferrin p
2	53	80.3	708	2 JC2323	lactoferrin - goat
3	50	75.8	33	3 S52107	lactoferrin - sheep
4	44	66.7	707	1 A28438	lactoferrin precu
5	43	65.2	4568	2 T08030	dynein beta heavy
6	40	60.6	275	2 T22597	hypothetical prote
7	40	60.6	932	2 T28820	hypothetical prote
8	39	59.1	206	2 H97451	pyridoxamine 5'-ph
9	39	59.1	206	2 AB2670	pyridoxamine 5'-ph
10	39	59.1	208	2 AG3441	probable pyridoxam
11	38	57.6	289	2 G86403	33.3K hypothetical
12	38	57.6	515	2 T00510	probable cytochrom
13	38	57.6	543	2 T00513	cytochrome P450 ho
14	38	57.6	1135	2 T14803	phytochrome C - so
15	37	56.1	85	2 AG0794	polymyxin B resist
16	37	56.1	121	2 AB3147	hypothetical prote
17	37	56.1	255	2 B87515	signal peptidase I
18	37	56.1	433	2 T32605	hypothetical prote
19	37	56.1	489	2 C70555	probable monooxyge
20	37	56.1	584	2 C84325	hypothetical prote
21	36	54.5	235	2 T38440	flt3 ligand - huma
22	36	54.5	275	1 JC1113	interleukin-2 rece
23	36	54.5	275	1 S07442	interleukin-2 rece
24	36	54.5	456	2 C86624	hypothetical prote
25	36	54.5	456	2 H72000	hypothetical prote
26	36	54.5	1391	2 T20642	hypothetical prote
27	36	54.5	1397	2 B87998	protein F09C3.1 li
28	35	53.0	124	2 C96582	F1511.22 (imported
29	35	53.0	220	1 S36092	pyridoxamine-phosp

ALIGNMENTS

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A51169; A31000; S74

R/Cho, Y.

Submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237

R/Rey, M.M.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148; T, 150-422, C, 424-711 <REY>

A/Cross-references: EMBL:X53961; NID:g34415; PIDN:CAA37914.1; PID:g34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactofer

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, N.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412

R/Stowell, K.W.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <ST1>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-26, X, 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A;Reference number: S07160; MUID:88001031; PMID:3477300
 A;Accession: S07160
 A;Molecule type: mRNA
 A;Residues: 436-487, 'A', 489-711 <RAD>
 A;Cross-references: EMBL:M18642; NID:G186815; PIDN:AAA86665.1; PID:G386855
 R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A;Reference number: A61169; MUID:9135214; PMID:1674448
 A;Accession: A61169
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 3-701, 'SWKPNV' <PAN>
 A;Experimental source: normal breast tissue
 R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
 Eur. J. Biochem. 145, 659-666, 1984
 A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
 A;Reference number: A31000; MUID:85076667; PMID:6510420
 A;Accession: A31000
 A;Molecule type: protein
 A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
 A;Note: this is the final paper in a series
 R;Houen, G.; Hoegedal, E.V.; Barkholt, V.; Norskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminoethyl affinity
 A;Reference number: S74119; MUID:97054624; PMID:8898921
 A;Accession: S74119
 A;Molecule type: protein
 A;Residues: 'Q', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A;Experimental source: neutrophil granulocytes
 C;Genetics:
 A;Gene: GDB:LTF
 A;Cross-references: GDB:119368; OMIM:150210
 A;Map position: 3q21-3q23
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein; iron binding; milk
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-711/Product: lactotransferrin #status experimental <MAT>
 F;21-356/Domain: transferrin repeat homology <TRH2>
 F;360-699/Domain: transferrin repeat homology <TRH2>
 F;29-65, 39-56, 135-218, 177-190, 201, 251-265, 503-697, 595-609/Disulfide bonds: #status e
 F;157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat

Query Match 97.0%; Score 64; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00083;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRMKVR 12
 DB 39 CFQWQRMKVR 50
 RESULT 2
 JC2323
 lactoferrin - goat
 C;Species: Capra aegagrus hircus (domestic goat)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C;Accession: JC2323
 R;Le Provost, F.; Noart, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A;Reference number: JC2323; MUID:94380047; PMID:8093048
 A;Accession: JC2323
 A;Molecule type: mRNA
 A;Residues: 1-708 <LEP>
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein
 F;359-696/Domain: transferrin repeat homology <TRH2>
 F;252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.3%; Score 53; DB 2; Length 708;
 Best Local Similarity 72.7%; Pred. No. 0.083;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRMKRV 11
 DB 38 CYQWQRMKRL 48
 RESULT 3
 S52107
 lactoferrin - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
 C;Accession: S52107
 R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
 Biochim. Biophys. Acta 1243, 25-32, 1995
 A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet
 A;Reference number: S52107; MUID:95127729; PMID:7827104
 A;Accession: S52107
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-33 <QIA>
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication
 Query Match 75.8%; Score 50; DB 2; Length 33;
 Best Local Similarity 63.6%; Pred. No. 0.016;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQRMKRV 11
 DB 19 CYQWQRMKRL 29
 RESULT 4
 A28438
 lactoferrin precursor - mouse
 N;Alternate names: lactotransferrin
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A28438; A41205
 R;Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secr
 A;Reference number: A92596; MUID:87280033; PMID:3611056
 A;Accession: A28438
 A;Molecule type: mRNA
 A;Residues: 3-707 <PEN>
 A;Cross-references: EMBL:J03298
 R;Liu, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A;Reference number: A41205; MUID:92042099; PMID:1939212
 A;Accession: A41205
 A;Molecule type: DNA
 A;Residues: 1-15 <LIU>
 A;Cross-references: GB:M74778
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: duplication; glycoprotein
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-707/Product: lactotransferrin #status predicted <MAT>
 F;358-695/Domain: transferrin repeat homology <TRH2>
 F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 66.7%; Score 44; DB 1; Length 707;
 Best Local Similarity 63.6%; Pred. No. 3.6;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQRMKRV 11
 DB 37 CLRWQNMKRV 47

```

RESULT 5
T08030
dynein beta heavy chain - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C:Accession: T08030
R:Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A:Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A:Reference number: Z16302; MUID:94274778; PMID:8006077
A:Accession: T08030
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4568 <MT>
A:Cross-references: EMBL:U02963; NID:9409965; PIDN:AAA19956.1; PID:G514215
A:Experimental source: strain 2igr
C:Genetics:
A:Gene: ODA4
A:Map position: IX
A:Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
3334/3; 3686/3; 3882/3; 4240/3
C:Superfamily: dynein heavy chain, ciliary
C:Keywords: nucleotide binding; P-loop
F:1919-1926/Region: nucleotide-binding motif A (P-loop)
F:2202-2209/Region: nucleotide-binding motif A (P-loop)
F:2530-2537/Region: nucleotide-binding motif A (P-loop)
Query Match 65.2%; Score 43; DB 2; Length 4568;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFQWRXMRKVR 12
DB 1852 CFQWQSLEYIQ 1863

RESULT 6
T22597
Hypothetical protein F53H4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T22597
R:Dobson, R.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19587
A:Accession: T22597
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <WIL>
A:Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
A:Experimental source: clone F53H4
C:Genetics:
A:Gene: CESP:F53H4.4
A:Map position: X
A:Introns: 67/1; 153/1
C:Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
Query Match 60.6%; Score 40; DB 2; Length 275;
Best Local Similarity 63.6%; Pred. No. 7.8;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 FQWRXMRKVR 12
DB 262 FQWKISMRKTR 272

RESULT 7
T28820
Hypothetical protein F07C3.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T28820
R:Pavello, A.; Gattung, S.
Submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid F07C3.
A:Reference number: Z20528
A:Accession: T28820
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-932 <FAV>
A:Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
A:Experimental source: strain Bristol N2; clone F07C3
C:Genetics:
A:Gene: CESP:F07C3.1
A:Map position: 5
A:Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 595/3;
Query Match 60.6%; Score 40; DB 2; Length 932;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 FQWRXMRKVR 12
DB 579 FQWRXMRKVR 589

RESULT 8
H97451
Pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (str
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: H97451
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, P.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:11743194
A:Accession: H97451
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:G15155733; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_1381
A:Map position: circular chromosome
C:Superfamily: pyridoxamine-phosphate oxidase
Query Match 59.1%; Score 39; DB 2; Length 206;
Best Local Similarity 50.0%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 CFQWRXMRKVR 12
DB 88 CFHWKSLRRQVR 99

RESULT 9
AB2670
Pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Du
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: AB2670
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AB2670
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <KUR>

```

A;Cross-references: GB:AE008688; PIDN:AAL41776.1; PID:g17739129; GSPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: pdxH
 A;Map position: circular chromosome
 C;Superfamily: pyridoxamine-phosphate oxidase

Query Match 59.1%; Score 39; DB 2; Length 206;
 Best Local Similarity 50.0%; Pred. No. 9;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
 |||:|:
 Db 88 CFHWKSLRRQVR 99

RESULT 10
 AG3441
 Probable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - Brucella melitensis (s
 C;Species: Brucella melitensis
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
 C;Accession: AG3441
 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,
 ; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A;Reference number: AD3252; PMID:11756688
 A;Accession: AG3441
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-208 <KUR>
 A;Cross-references: GB:AE008917; PIDN:AAL52698.1; PID:g17983525; GSPDB:GN00190
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BWE11517
 A;Map position: I
 C;Superfamily: Pyridoxamine-phosphate oxidase
 C;Keywords: oxidoreductase

Query Match 59.1%; Score 39; DB 2; Length 208;
 Best Local Similarity 50.0%; Pred. No. 9;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
 |||:|:
 Db 90 CFHWKSLRRQVR 101

RESULT 11
 G86403
 33.3K hypothetical protein F28L5.13 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
 C;Accession: G86403
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; PMID:21016719; PMID:11130712
 A;Accession: G86403
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-269 <STO>
 A;Cross-references: GB:AE005172; NID:g10998925; PIDN:AG25065.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1

Query Match 57.6%; Score 38; DB 2; Length 289;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQXMRKVR 12
 |||:|:
 Db 8 CFTWEYARHVR 19

RESULT 12
 T00510
 Probable cytochrome P450 At2g23220 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
 C;Accession: T00510; A84622
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau
 submitted to the EMBL Data Library, November 1997
 A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
 A;Reference number: Z14164
 A;Accession: T00510
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-515 <ROU>
 A;Cross-references: EMBL:AC002391; NID:g2642427; FID:g2642441
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; PMID:20083487; PMID:10617197
 A;Accession: A84622
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-515 <STO>
 A;Cross-references: GB:AE002093; NID:g2642441; PIDN:AAB87109.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g23220; T20D16.15
 A;Map position: 2
 A;Introns: 182/3; 310/3
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: heme; iron; metalloprotein
 F;312-471/Domain: cytochrome P450 homology <P45>
 F;449/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 57.6%; Score 38; DB 2; Length 515;
 Best Local Similarity 83.3%; Pred. No. 33;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQ 6
 |||:|:
 Db 469 CFQWQ 474

RESULT 13
 T00513
 Cytochrome P450 homolog At2g23190 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
 C;Accession: T00513; F84621
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau
 submitted to the EMBL Data Library, November 1997
 A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
 A;Reference number: Z14164
 A;Accession: T00513
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-543 <ROU>
 A;Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642444
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: R84420; MUID:20083487; PMID:10617197
A/Accession: F84621
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-543 <STO>
A/Cross-references: GB:AB002093; NID:g2642444; PIDN:AAB87112.1; GSPDB:GN00139
C/Genetics:
A/Gene: T20D16.18; At2g23190
A/Map position: 2
A/Introns: 211/3; 339/3
A/Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
A/Keywords: heme; iron; metalloprotein
A/341-500/Domain: cytochrome P450 homology <P45>
A/478/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 57.6%; Score 38; DB 2; Length 543;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XY 1 CFQWQR 6
|||
DB 498 CFQWQR 503

RESULT 14
T14803
phytochrome C - sorghum
A/Species: Sorghum bicolor (sorghum)
A/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
A/Accession: T14803
A/Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet,
submitted to the EMBL Data Library, April 1996
A/Reference number: Z18186
A/Accession: T14803
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1135 <CHI>
A/Cross-references: EMBL:U56731; NID:g1800218; PID:g1800219
C/Genetics:
A/Gene: PHYC
A/Superfamily: phytochrome; phytochrome homology
A/Keywords: chromoprotein; dimer; photoreceptor; phytochromobilin; transcription regulat
A/65-581/Domain: phytochrome homology <PHY>
A/321/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 57.6%; Score 38; DB 2; Length 1135;
Best Local Similarity 36.4%; Pred. No. 69;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

XY 1 CFQWQRXMRKV 11
|||
DB 775 CLEWKNXMQKI 785

RESULT 15
AG0794
polymyxin B resistance protein [imported] - Salmonella enterica subsp. enterica serovar
A/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
A/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
A/Accession: AG0794
A/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
h, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
A/413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; PMID:11677608
A/Accession: AG0794
A/Status: Preliminary
A/Molecule type: DNA

A/Residues: 1-85 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD07537.1; PID:g16503529; GSPDB:GN00176
C/Genetics:
A/Gene: pmrD

Query Match 56.1%; Score 37; DB 2; Length 85;
Best Local Similarity 60.0%; Pred. No. 8.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRXMRK 10
|||
DB 74 CDEWQLTRK 83

Search completed: February 21, 2003, 08:02:45
Job time : 11.6047 secs

GenCore version 5.1.3
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DM protein - protein search, using sw model

Run on: February 21, 2003, 07:28:06 ; Search time 5.2093 seconds
(without alignments)
95.544 Million cell updates/sec

Title: US-09-743-107B-90
Perfect score: 66
Sequence: 1 CFQQRXMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	97.0	711	1 TRFL_HUMAN	P02788 homo sapien
2	53	80.3	708	1 TRFL_CAMDR	Q9tumo camelus dro
3	53	80.3	708	1 TRFL_CAPHI	Q29477 capra hircu
4	44	66.7	707	1 TRFL_MOUSE	P08071 mus musculu
5	43	65.2	4568	1 DYHB_CHLRE	Q39565 chlamydomon
6	39	59.1	695	1 TRFL_HORSE	Q77811 equus cabal
7	38	57.6	292	1 NLA_DROME	Q9x218 drosophila
8	38	57.6	1135	1 PHYC_SORBI	P93528 sorghum bic
9	37	56.1	85	1 PMRD_SALTY	P37589 salmonella
10	37	56.1	146	1 RPOB_LIBAP	P41187 liberibacte
11	36	54.5	235	1 FL3L_BOVIN	P49771 homo sapien
12	36	54.5	275	1 IL2A_SHEEP	P12342 bos taurus
13	36	54.5	275	1 IL2A_SHEEP	P26898 ovis aries
14	36	54.5	1137	1 PHYC_ORISA	Q92w19 oryza sativ
15	36	54.5	1179	1 ATX1_ARATH	Q9lt02 arabidopsis
16	35	53.0	270	1 PDHX_MYXXA	P21159 myxococcus
17	35	53.0	306	1 BUB2_YEAST	P26448 saccharomyc
18	35	53.0	435	1 DCOR_PANRE	P49725 panagrellus
19	35	53.0	502	1 C911_ARATH	Q9f655 arabidopsis
20	35	53.0	783	1 YNR2_CAEEL	Q21388 caenorhabdi
21	35	53.0	2594	1 7LES_DROVI	P20806 drosophila
22	34	51.5	211	1 LOLB_VIBCH	P57070 vibrio chol
23	34	51.5	227	1 CHEZ_PSEAE	Q51434 pseudomonas
24	34	51.5	275	1 VA16_VACCV	P16710 vaccinia vi
25	34	51.5	378	1 RADA_CHLMU	P20993 vaccinia vi
26	34	51.5	455	1 TLCE_RICPR	Q9pk96 chlamydia m
27	34	51.5	500	1 TRFL_EUBBU	O05962 rickettsia
28	34	51.5	708	1 TRFL_EUBBU	Q77698 bubalus bub
29	34	51.5	765	1 Y008 HUMAN	Q15398 homo sapien
30	34	51.5	962	1 YXB7_SCHPO	Q10201 schizosacch
31	33	50.0	159	1 Y1CN_ECOLI	P31439 escherichia
32	33	50.0	272	1 IL2A_HUMAN	P01589 homo sapien
33	33	50.0	377	1 VA16_VARV	P33841 variola vir

34	33	50.0	428	1 SYH_CHLMU	Q9pij9 chlamydia m
35	33	50.0	475	1 YEB1_HAEIN	P44933 haemophilus
36	33	50.0	456	1 MSS1_SCHPO	Q9uce7 schizosacch
37	33	50.0	506	1 AER_ECOLI	P50466 escherichia
38	33	50.0	704	1 TRFL_PIG	P14632 sus scrofa
39	33	50.0	1131	1 PHY_PINSY	Q41046 pinus sylve
40	33	50.0	1213	1 T2D2_DROME	Q24325 drosophila
41	33	50.0	1293	1 XPC_DROME	Q24595 drosophila
42	33	50.0	2554	1 7LES_DROME	P13368 drosophila
43	32	48.5	77	1 NULM_ASCSU	P24874 ascaris suu
44	32	48.5	137	1 YEDD_ECOLI	P31063 escherichia
45	32	48.5	141	1 YEDD_SALTY	Q06399 salmonella

ALIGNMENTS

RESULT 1
TRFL_HUMAN
ID AC P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H1Z3; Q96KZ4;
AC Q96KZ5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;
DE Lactoferrin B; Lactoferrin C].
GN LTF OR LF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90384839; PubMed=2402455;
RA Rev M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX Cho Y.Y.;
RL Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Connely O.M.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX Liang Q., Jimenez-Flores R., Richardson T.;
RT "Molecular cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RT "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX Cheng H., Chen X., Huan L.;
RT "cDNA cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE-Mammary gland.
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.B.;
RT "Nucleotide sequence of human lactoferrin cDNA";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RT Metz-Boutigue M.-H., Jolles J., Jolles P.;
RL Legrand D., Spik G., Montreuil J., Jolles P.;
RN "Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins";
RX Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RT Jolles P.;
RN "The present state of the human lactotransferrin sequence. Study and
alignment of the cyanogen bromide fragments and characterization of
N- and C-terminal domains";
RX Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RT Jolles P.;
RN "An 88 amino acid long C-terminal sequence of human
lactotransferrin";
RX FEBS Lett. 142:107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
expression of mRNA during normal and leukemic myelopoiesis";
RX Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhoj M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RT Gao L., la Bastide M., Kaplan M., Greco T., Touchman J., Muzny D.,
RN Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RT Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RN Sadrilpanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
and refinement at 2.8-A resolution";
RX J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
resolution";
RX Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RT Baker E.N.;
RN "Mutagenesis of the histidine ligand in human lactoferrin: iron
binding properties and crystal structure of the histidine-
253->-methionine mutant";
RX Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
awamori";
RX Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
and analysis of ligand-induced conformational change";
RX Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioic antagonist peptides derived
from human lactoferrin";
RX Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RT Cumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RN Sugar J., Kumaranickavel G., Munier F., Schorderet D.P.,
RA El Matiri L., Iwata F., Kaiser-Kupfer M., Negata M., Nakayasu K.,
RT Hejtmancik J.F., Teng C.T.;
RN "Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene";
RX Mol. Vision 4:31-32(1998).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
CC -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC -----
DR EMBL; X53961; CAA37914.1; -
DR EMBL; U07643; AAB60324.1; -
DR EMBL; M91150; AAA36159.1; -
DR EMBL; M83202; AAA59511.1; -
DR EMBL; M83205; AAA86656.1; -
DR EMBL; M18642; AAA86655.1; -
DR EMBL; AF332168; AAG48753.1; -
DR EMBL; BC015822; AAH15822.1; -
DR EMBL; BC015823; AAH15823.1; -
DR EMBL; M73700; AAA59479.1; -
DR EMBL; X52941; CAA37116.1; -
DR EMBL; U95626; AAB57795.1; -
DR PIR; S11228; TPFHUL.
DR PDB; 1LCF; 31-AUG-94.
DR PDB; 1LCT; 31-OCT-93.
DR PDB; 1LFG; 31-JUL-94.
DR PDB; 1LFH; 31-OCT-93.
DR PDB; 1LFI; 31-OCT-93.
DR PDB; 1LGB; 31-AUG-94.
DR PDB; 1LGC; 31-AUG-94.
DR PDB; 1BKA; 08-NOV-96.
DR PDB; 1DSN; 08-MAR-96.
DR PDB; 1HSB; 12-MAR-97.
DR PDB; 1VFD; 21-APR-97.

Query Match 97.0%; Score 64; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.00024;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQXMKVR 12
 DB 39 CFQWQXMKVR 50

RESULT 2
 ID TRFL_CAMDR STANDARD; PRT; 708 AA.
 AC Q9TUM0; Q9MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 LN Lf.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R.; Ackermann M.; Farah Z.; Puhan Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M.; Srinivasan A.; Singh R.; Sahani M.S.; Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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CC EMBL; AJ131674; CAB53387.1; -
 CC EMBL; AF165879; AAF82241.1; -
 CC HSRF; O77811; 151X.
 CC InterPro; IPR001156; Transferrin.
 CC Pfam; PF00405; transferrin; 2.
 CC PRINTS; PR00422; TRANSFERRIN.
 CC SMART; SM00094; TR_FER; 2.
 CC PROSITE; PS00205; TRANSFERRIN 1; 2.
 CC PROSITE; PS00206; TRANSFERRIN 2; 2.
 CC PROSITE; PS00207; TRANSFERRIN 3; 2.
 CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 CC Signal.
 CC CHAIN 1 19 BY SIMILARITY.
 CC REPEAT 20 708 LACTOTRANSFERRIN.
 CC REPEAT 20 363 1.
 CC REPEAT 364 708 2.
 CC DISULFID 28 64 BY SIMILARITY.
 CC DISULFID 38 55 BY SIMILARITY.
 CC DISULFID 134 217 BY SIMILARITY.
 CC DISULFID 176 192 BY SIMILARITY.
 CC DISULFID 189 200 BY SIMILARITY.
 CC DISULFID 250 264 BY SIMILARITY.
 CC DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79 IRON 1 (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 261 261 F -> S (IN REF. 2).
 FT CONFLICT 304 304 G -> A (IN REF. 2).
 FT CONFLICT 330 330 S -> P (IN REF. 2).
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
 FT CONFLICT 506 506 L -> F (IN REF. 2).
 FT CONFLICT 609 609 A -> P (IN REF. 2).
 FT CONFLICT 642 642 R -> Q (IN REF. 2).
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;
 Query Match 80.3%; Score 53; DB 1; Length 708;
 Best Local Similarity 75.0%; Pred. No. 0.025;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CFQWQXMKVR 12
 DB 38 CAQWQRMKKVR 49
 RESULT 3
 ID TRFL_CAPHI STANDARD; PRT; 708 AA.
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 LN Lf.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T.; Yu S.; Kim S.; Lee K.; Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA MEDLINE=94380047; PubMed=8093048;
 RA "le Provost F.; Nocart M.; Guerin G.; Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 RT relevant locus to bovine U12 syntenic group.";
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.

I REPEAT 358 707 2.
 I DISULFID 27 63 BY SIMILARITY.
 I DISULFID 37 54 BY SIMILARITY.
 I DISULFID 133 216 BY SIMILARITY.
 I DISULFID 175 191 BY SIMILARITY.
 I DISULFID 188 199 BY SIMILARITY.
 I DISULFID 249 263 BY SIMILARITY.
 I DISULFID 366 398 BY SIMILARITY.
 I DISULFID 376 389 BY SIMILARITY.
 I DISULFID 423 702 BY SIMILARITY.
 I DISULFID 443 665 BY SIMILARITY.
 I DISULFID 475 550 BY SIMILARITY.
 I DISULFID 499 693 BY SIMILARITY.
 I DISULFID 509 523 BY SIMILARITY.
 I DISULFID 520 533 BY SIMILARITY.
 I DISULFID 591 605 BY SIMILARITY.
 I DISULFID 643 648 BY SIMILARITY.
 I METAL 78 78 IRON 1 (BY SIMILARITY).
 I METAL 110 110 IRON 1 (BY SIMILARITY).
 I METAL 210 210 IRON 1 (BY SIMILARITY).
 I METAL 271 271 IRON 1 (BY SIMILARITY).
 I METAL 413 413 IRON 2 (BY SIMILARITY).
 I METAL 451 451 IRON 2 (BY SIMILARITY).
 I METAL 544 544 IRON 2 (BY SIMILARITY).
 I METAL 613 613 IRON 2 (BY SIMILARITY).
 I BINDING 139 139 ANION (POTENTIAL).
 I BINDING 481 481 ANION (POTENTIAL).
 I CARBOHYD 118 118 N-LINKED (GLCNAC).
 I CARBOHYD 494 494 N-LINKED (GLCNAC).
 I CONFLICT 1 2 MR -> IQG (IN REF. 1).
 I CONFLICT 25 25 R -> Q (IN REF. 2).
 I CONFLICT 82 82 M -> L (IN REF. 2).
 I CONFLICT 359 359 S -> T (IN REF. 2).
 I CONFLICT 382 382 A -> D (IN REF. 1).
 I CONFLICT 449 449 E -> G (IN REF. 2).
 I CONFLICT 629 629 L -> V (IN REF. 1).
 I SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;
 Y 1 CFQWQXMRKV 11
 b 37 CLRQWQXMRKV 47
 RESULT 5
 D_YVHB CHLRE STANDARD; PRT; 4568 AA.
 C Q39565; 1997 (Rel. 35, Created)
 I 01-NOV-1997 (Rel. 35, Last sequence update)
 I 30-MAY-2000 (Rel. 39, Last annotation update)
 E Dynein beta chain, flagellar outer arm.
 N ODA4 OR ODA-4 OR SUP1.
 S Chlamydomonas reinhardtii.
 C Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 C Chlamydomonadaceae; Chlamydomonas.
 X NCBI_TaxID=3055;
 N [1]
 P SEQUENCE FROM N.A.
 C STRAIN=21GT;
 X MEDLINE=94274778; PubMed=8006077;
 I Mitchell D.R.; Brown K.S.;
 I "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes."
 L J. Cell Sci. 107:635-644(1994).
 C -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES. DYNEIN HAS ATPASE ACTIVITY.
 C -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.

CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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 CC EMBL; U02963; AAA19956.1;
 DR InterPro; IPR004273; Dynein heavy.
 DR Pfam; PF03028; Dynein heavy; 1.
 KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
 KW Coiled coil. 277 293
 FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
 FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
 FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
 FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
 FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
 FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
 FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
 FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
 FT DOMAIN 3648 3728 ATP (POTENTIAL).
 FT NP_BIND 1919 1926 ATP (POTENTIAL).
 FT NP_BIND 2202 2209 ATP (POTENTIAL).
 FT NP_BIND 2530 2537 ATP (POTENTIAL).
 FT NP_BIND 2879 2886 ATP (POTENTIAL).
 SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;
 Query Match 65.2%; Score 43; DB 1; Length 4568;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQXMRKV 12
 DB 1852 CFQWQXMRKV 12
 RESULT 6
 TRFL_HORSE STANDARD; PRT; 695 AA.
 ID TRFL_HORSE
 AC O77811;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).
 GN LTF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OK NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "cDNA sequence of mare lactoferrin."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Milk;
 RX MEDLINE=99296631; PubMed=10366507;
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A resolution."
 RL J. Mol. Biol. 289:303-317(1999).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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EMBL; AJ010930; CAA09407.1; --
PDB; 1BIX; 02-DEC-98.
PDB; 1B7U; 02-FEB-99.
PDB; 1B7Z; 02-FEB-99.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
PROSITE; PS00205; TRANSFERRIN_1; 2.
PROSITE; PS00206; TRANSFERRIN_2; 1.
PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal; 3D-structure.
FT SIGNAL 1 6
FT CHAIN <1 6 LACTOTRANSFERRIN.
FT REPEAT 7 350
FT REPEAT 351 695
FT DISULFID 15 51
FT DISULFID 25 42
FT DISULFID 121 204
FT DISULFID 163 179
FT DISULFID 186 189
FT DISULFID 176 187
FT DISULFID 237 251
FT DISULFID 354 386
FT DISULFID 364 377
FT DISULFID 411 690
FT DISULFID 431 653
FT DISULFID 463 538
FT DISULFID 487 681
FT DISULFID 497 511
FT DISULFID 508 521
FT DISULFID 579 593
FT DISULFID 631 636
FT METAL 66 66
FT METAL 98 98
FT METAL 198 198
FT METAL 259 259
FT METAL 401 401
FT METAL 439 439
FT METAL 532 532
FT METAL 601 601
FT BINDING 127 127
FT BINDING 469 469
FT CARBOHYD 143 143
FT CARBOHYD 287 287
FT CARBOHYD 482 482
SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B16SD CRC64;
Query Match 59.1%; Score 39; DB 1; Length 695;
Best Local Similarity 58.3%; Pred. No. 9.3;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFQWQRXMKVR 12
| : : : : :
Db 25 CAKFRNMKVR 36
RESULT 7
ID NLA DROME
AC Q9XZL8; Q9V391; PRT; 292 AA.
DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nebula protein.
GN NLA OR C60702.
OS Drosophila melanogaster (Fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN SEQUENCE FROM N.A.
RP McCormick A.V., Goldberg M.L.;
RT "Gene required for elongation of meiosis I spindle in Drosophila females."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Berkley;
RX MEDLINE=2019606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Flossler C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko F., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang Z.-Y.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
CC -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
CC -----
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EMBL; AF147700; AAD33987.1; --
EMBL; AE003712; AAF55285.1; --
DR FlyBase; Fegno0026629; nla.
DR SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
SQ

Query Match 57.6%; Score 38; DB 1; Length 292;
 Best Local Similarity 54.5%; Pred. No. 6;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Y 2 FQWQXVXKVR 12
 |||||:
 150 FQWLSFRLR 160

RESULT 8
 HYC_SORBI
 D -HYC_SORBI STANDARD; PRT; 1135 AA.
 C P93528;
 Y 16-OCT-2001 (Rel. 40, Created)
 Y 16-OCT-2001 (Rel. 40, Last sequence update)
 Y 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phytochrome C.
 IN PHYC.
 S Sorghum bicolor (Sorghum) (Sorghum vulgare).
 C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 C Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 C Panicoideae; Andropogoneae; Sorghum.
 X NCBI_TaxID=4558;
 [1]
 SEQUENCE FROM N.A.
 P MEDLINE=97198556; PubMed=9046599;
 A Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
 A Morgan P.W., Mullet J.E.;
 T "The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
 T phytochrome B.";
 L Plant Physiol. 113:611-619 (1997).
 C -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
 C ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
 C MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
 C ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
 C PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
 C RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
 C RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
 C GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RUBULOSE-
 C BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
 C PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS THE
 C EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY
 C SIMILARITY).
 C -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 C -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
 C -!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
 C -!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
 C -!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
 C -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
 C
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 C or send an email to license@isb-sib.ch).
 C
 C EMBL; U56731; AAB41399.1;
 R InterPro; IPR003594; ATPbind_ATPase.
 R InterPro; IPR003018; GAF.
 R InterPro; IPR004359; HIS_KIN_sig.
 R InterPro; IPR003661; HIS_KIN.
 R InterPro; IPR001610; PAC.
 R InterPro; IPR000014; PAS_domain.
 R InterPro; IPR001294; Phytochrome.
 R Pfam; PF00360; phytochrome; 1.
 R Pfam; PF00512; signal; 1.
 R Pfam; PF00989; PAS; 2.
 R Pfam; PF01590; GAF; 1.
 R Pfam; PF02518; HATPase_c; 1.
 R PRINTS; PR01033; PHYTOCHROME.
 R SMART; SM00065; GAF; 1.

DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; HSKA; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR TIGRFRAME; TIGR00229; sensory_box; 2.
 DR PROSITE; PSS0109; HIS_KIN; 1.
 DR PROSITE; PSS0112; PAS; 2.
 DR PROSITE; PSS0245; PHYTOCHROME_1; FALSE_NEG.
 DR PROSITE; PSS0046; PHYTOCHROME_2; 1.
 KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
 KW Repeat; Multigene family.
 FT DOMAIN 618 688 PAS 1.
 FT DOMAIN 748 822 PAS 2.
 FT DOMAIN 902 1122 HISTIDINE KINASE.
 FT BINDING 321 321 CHROMOPHORE (BY SIMILARITY).
 SQ SEQUENCE 1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;

Query Match 57.6%; Score 38; DB 1; Length 1135;
 Best Local Similarity 36.4%; Pred. No. 23;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CFQWQXVXKVR 11
 |||||:
 Db 775 CLEWKAQKI 785

RESULT 9
 PMRD_SALTY
 ID PMRD_SALTY STANDARD; PRT; 85 AA.
 AC P37589;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Polymyxin B resistance protein pmrD.
 GN PMRD OR STM2304.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE=94266712; PubMed=8206837;
 RA Roland K.L., Esther C.R., Spitznagel J.K.;
 RT "Isolation and characterization of a gene, pmrD, from Salmonella
 RT typhimurium that confers resistance to polymyxin when expressed in
 RT multiple copies.";
 RL J. Bacteriol. 176:3589-3597 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Anderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856 (2001).
 CC -!- FUNCTION: CONFERS RESISTANCE TO POLYMYXIN B. POLYMYXIN RESISTANCE
 CC MAY BE MEDIATED BY AN INTERACTION BETWEEN PMRA OR A PMRA-REGULATED
 CC GENE PRODUCT AND PMRD.
 CC
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 CC
 CC EMBL; U02281; AAA21322.1; -.

ID	FL3L_HUMAN	STANDARD;	PRT;	235 AA.
AC	P49771;			
CD	01-OCT-1996 (Rel. 34, Created)			
AD	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DT	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3L).			
DE	Flt3LG.			
DE	Homo sapiens (Human).			
GN	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OS	NCBI_TaxID=9606;			
OC	[1]			
OR	SEQUENCE FROM N.A.			
RP	MEDLINE=94115428; PubMed=814581;			
RP	Hannun C., Culppepper J., Campbell D., McLanahan T., Zurawski S., Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J., Duda G., Martina N., Peterson D., Menon S., Shanafelt A., Muench M., Kelnher G., Namikawa R., Rennick D., Roncarolo M.G., Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;			
RA	"Ligand for Flt3/Flk2 receptor tyrosine kinase regulates growth of haematopoietic stem cells and is encoded by variant RNAs.";			
RT	Nature 368:643-648(1994).			
RL	[2]			
RL	SEQUENCE FROM N.A.			
RP	MEDLINE=94235842; PubMed=8180375;			
RP	Lyman S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S.S., Downey H., Spiett R.R., Beckmann M.P., McKenna H.J.;			
RA	"Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoietic progenitor cells.";			
RT	Blood 83:2795-2801(1994).			
RL	[3]			
RL	SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.			
RP	MEDLINE=96032581; PubMed=7566977;			
RP	Lyman S.B., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S.;			
RA	"Structural analysis of human and murine flt3 ligand genomic loci.";			
RT	Oncogene 11:1165-1172(1995).			
RL	[4]			
RL	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).			
RP	MEDLINE=20343011; PubMed=10881197;			
RP	Savvides S.N., Boone T., Karplus P.A.;			
RA	"Flt3 ligand structure and unexpected commonalities of helical bundles and cysteine knots.";			
RT	Nat. Struct. Biol. 7:486-491(2000).			
RL	-!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.			
CC	-!- SUBUNIT: Homodimer (isoform 2).			
CC	-!- SUBCELLULAR LOCATION: type I membrane protein (isoform 1); secreted (isoform 2).			
CC	-!- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here) and 2/soluble; are produced by alternative splicing.			
CC	-----			
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CC	-----			
CC	EMBL; U04806; AAA17999.1; -			
DR	EMBL; U03858; AAA19825.1; -			
DR	EMBL; U29874; AAA30949.1; -			
DR	EMBL; U29874; AAA30950.1; -			
DR	PDB; 1ETE; 09-JUN-00.			
DR	GeneW; HGNC:3766; FLT3LG.			
DR	MIM; 600007; -			
DR	InterPro; IPR004213; Flt3 lig.			
DR	Pfam; PF02947; Flt3 lig; 1.			
DR	Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;			
KW	3D-structure.			

FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 235 SL CYTOKINE.
 FT DOMAIN 27 184 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 185 205 POTENTIAL.
 FT DOMAIN 206 235 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 30 111
 FT DISULFID 30 153
 FT DISULFID 119 158
 FT CARBOHYD 126 126
 FT CARBOHYD 149 149
 FT VARSPLIC 161 178
 FT VARSPLIC 179 235
 FT VARSPLIC 179 235
 FT CONFLICT 72 72
 FT CONFLICT 72 72
 SQ SEQUENCE 235 AA; 26416 MW; 73895BF693B4CECF CRC64;
 Query Match 54.5%; Score 36; DB 1; Length 235;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 2Y 1 CFQWQRYMK 10
 3b 204 CLHWQRTERR 213
 RESULT 12
 IL2A_BOVIN STANDARD; PRT; 275 AA.
 ID IL2A_BOVIN STANDARD; PRT; 275 AA.
 AC P12342;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
 DE subunit) (P55) (TAC antigen) (CD25).
 EN IL2RA.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88212503; PubMed=2835311;
 RA Weinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
 RA Reeves R., Magnuson J.A.;
 RT "Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
 RL Immunology 63:603-610(1988).
 RN [2]
 RP SEQUENCE OF 1-21 FROM N.A.
 RX MEDLINE=96116968; PubMed=8563178;
 RA Yoo J., de Leon F.A., Stone R.T., Beattie C.W.;
 RT "Cloning and chromosomal assignment of the bovine interleukin-2
 receptor alpha (IL-2R alpha) gene.";
 RL Mamm. Genome 6:751-753(1995).
 CC -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
 CC -!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
 CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
 CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
 CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
 CC WITH A GAMMA CHAIN.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; M20818; AAA51414.1; --
 CC EMBL; U24226; AAC48487.1; --

DR PIR; S07442; S07442.
 DR HSSP; P01569; IILM.
 DR InterPro; IPR000436; Sush1_SCR_CCP.
 DR Pfam; PF00084; sush1; 2.
 DR SMART; SM00032; CCP; 2.
 KW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sush1.
 FT SIGNAL 1 21
 FT CHAIN 22 275
 FT DOMAIN 22 243
 FT TRANSMEM 244 262
 FT DOMAIN 263 275
 FT DOMAIN 263 275
 FT DOMAIN 122 185
 FT DOMAIN 122 185
 FT DISULFID 24 64
 FT DISULFID 751 77
 FT DISULFID 123 168
 FT DISULFID 152 184
 FT CARBOHYD 80 80
 FT CARBOHYD 109 109
 FT CARBOHYD 109 109
 SQ SEQUENCE 275 AA; 31238 MW; 4901BBF9A4862390 CRC64;
 Query Match 54.5%; Score 36; DB 1; Length 275;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CFQWQRYMKVR 12
 Db 261 CLTWQKWKQR 272
 RESULT 13
 IL2A_SHEEP STANDARD; PRT; 275 AA.
 ID IL2A_SHEEP STANDARD; PRT; 275 AA.
 AC P28698;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
 DE subunit) (P55) (TAC antigen) (CD25).
 EN IL2RA.
 OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RA Verhagen A.A.;
 RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92241682; PubMed=1572550;
 RA Bujdosó R., Sargan D.R., Williamson M.L., McConnell I.;
 RT "Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa
 protein, CD25.";
 RL Gene 113:283-284(1992).
 CC -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
 CC -!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
 CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
 CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
 CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
 CC WITH A GAMMA CHAIN.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; M20818; AAA51414.1; --
 CC EMBL; U24226; AAC48487.1; --

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CC -----
DR ENBL; Z11560; CAA77652.1; -
DR ENBL; X60149; CAA42723.1; -
DR ENBL; A39167; CAA01447.1; -
DR PIR; S18910; S18910.
DR PIR; S18899; S18899.
DR PIR; JCI113; JCI113.
DR HSP; P01589; IILM.
DR InterPro; IPR000436; Sushi_scr_CCP.
DR Pfam; PF00084; sushi; 2.
DR SMART; SM00032; CCP; 2.
KW TRANSMEMBRANE; Glycoprotein; Receptor; Repeat; Signal; Sushi.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 262 POTENTIAL.
FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 78 SUSHI 1.
FT DOMAIN 122 185 SUSHI 2.
FT DISULFID 24 64 BY SIMILARITY.
FT DISULFID 751 77 BY SIMILARITY.
FT DISULFID 123 168 BY SIMILARITY.
FT DISULFID 152 184 BY SIMILARITY.
FT CARBOHYD 180 180 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 186 186 S -> T (IN REF. 2).
SQ SEQUENCE 275 AA; 30904 MW; 1101A2DESACS088 CRC64;

Query Match 54.5%; Score 36; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWQXMKVR 12
DB 261 CLTWQXWKQR 272

RESULT 14
PHYC_ORYSA
ID PHYC_ORYSA STANDARD; PRT; 1137 AA.
AC Q92W19; P93429;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome C.
GN PHYC.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Tahir M., Kanegae H., Takano M.;
RT "Phytochrome C (PHYC) gene in rice: isolation and characterization of
a complete coding sequence.";
RL (in) Plant Gene Register PGR98-210.
RN [2]
RP SEQUENCE OF 275-378 FROM N.A.
RX MEDLINE=97019052; PubMed=8865688;
RA Mathews S., Sharrock R.A.;
RT "The phytochrome gene family in grasses (Poaceae): a phylogeny and
evidence that grasses have a subset of the loci found in dicot
angiosperms.";
RL Mol. Biol. Evol. 13:1141-1150(1996).
CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-

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CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS
CC THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- PFM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; AB018442; BAA74448.1; -
CC ENBL; U61207; ABA41996.1; -
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR004359; HIS_KIN_sig.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001294; Phytochrome.
DR Pfam; PF00360; phytochrome; 1.
DR Pfam; PF00512; signal; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR01033; PHYTOCHROME.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HisKA; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR TIGRPFAMS; TIGR00229; sensory_box; 2.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0112; PAS; 2.
DR PROSITE; PS00245; PHYTOCHROME_1; 1.
DR PROSITE; PS0046; PHYTOCHROME_2; 1.
KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
KW Repeat; Multigene family.
FT DOMAIN 620 690 PAS 1.
FT DOMAIN 750 824 PAS 2.
FT DOMAIN 904 1124 HISTIDINE KINASE.
FT BINDING 322 322 CHROMOPHORE (BY SIMILARITY).
FT CONFLICT 279 279 F -> S (IN REF. 2).
FT CONFLICT 292 292 C -> S (IN REF. 2).
SQ SEQUENCE 1137 AA; 125982 MW; F2A520181CFE7B32 CRC64;

Query Match 54.5%; Score 36; DB 1; Length 1137;
Best Local Similarity 36.4%; Pred. No. 54;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQXMKV 11
DB 777 CLEWEMQKI 787.

RESULT 15
ATX1_ARATH
ID ATX1_ARATH STANDARD; PRT; 1179 AA.
AC Q9L702.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potential cation-transporting ATPase (EC 3.6.3.-).
GN AT5G23630 OR MQM1.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

C Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
C eurosids II; Brassicales; Brassicaceae; Arabidopsis.
X NCBI_TaxID=3702;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=cv. Columbia;
X MEDLINE=20181125; PubMed=10718197;
A Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
A Tabata S.;
T "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
T features of the regions of 3,076,755 bp covered by sixty P1 and TAC
T clones";
L DNA Res. 7:31-63(2000).
C -!- FUNCTION: INVOLVED IN TRANSPORT OF CATIONS (POTENTIAL).
C -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
C -!- SUBCELLULAR LOCATION: Integral membrane protein.
C -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
C (E1-E2 ATPASES). SUBFAMILY V.
C -----
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C -----
C EMBL; AB025633; BAA97238.1; -
C InterPro; IPR001757; ATPase_E1-E2.
R InterPro; IPR001454; Hlgase/hydriase.
R Pfam; PF00122; E1-E2 ATPase; 1.
R Pfam; PF00702; Hydrolase; 1.
R PRINTS; PR00119; CATATPASE.
R PROSITE; PS00154; ATPase_E1_E2; 1.
W Hydrolase; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
W Magnesium.
T DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
T TRANSMEM 21 42 POTENTIAL.
T DOMAIN 43 50 EXTRACELLULAR (POTENTIAL).
T TRANSMEM 51 71 POTENTIAL.
T DOMAIN 72 192 CYTOPLASMIC (POTENTIAL).
T TRANSMEM 193 215 POTENTIAL.
T DOMAIN 216 218 EXTRACELLULAR (POTENTIAL).
T TRANSMEM 219 238 POTENTIAL.
T DOMAIN 239 402 CYTOPLASMIC (POTENTIAL).
T TRANSMEM 403 422 POTENTIAL.
T DOMAIN 423 435 EXTRACELLULAR (POTENTIAL).
T TRANSMEM 436 453 POTENTIAL.
T DOMAIN 454 947 CYTOPLASMIC (POTENTIAL).
T TRANSMEM 948 967 POTENTIAL.
T DOMAIN 968 979 EXTRACELLULAR (POTENTIAL).
T TRANSMEM 980 997 POTENTIAL.
T DOMAIN 998 1013 CYTOPLASMIC (POTENTIAL).
T TRANSMEM 1014 1034 POTENTIAL.
T DOMAIN 1035 1059 EXTRACELLULAR (POTENTIAL).
T TRANSMEM 1060 1079 POTENTIAL.
T DOMAIN 1080 1092 CYTOPLASMIC (POTENTIAL).
T TRANSMEM 1093 1110 POTENTIAL.
T DOMAIN 1111 1128 EXTRACELLULAR (POTENTIAL).
T TRANSMEM 1129 1148 POTENTIAL.
T DOMAIN 1149 1178 CYTOPLASMIC (POTENTIAL).
T TRANSMEM 1175 1178 POLY-LYS.
T MOD_RES 491 491 PHOSPHORYLATION (BY SIMILARITY).
T METAL 812 812 MAGNESIUM (BY SIMILARITY).
T METAL 816 816 MAGNESIUM (BY SIMILARITY).
Q SEQUENCE 1179 AA; 131115 MW; 4A3B82D222A4D78 CRC64;
Query Match 54.5%; Score 36; DB 1; Length 1179;
Best Local Similarity 44.4%; Pred. No. 56;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Y 1 CFQWQXMR 9
|:|:|:|

Db 1144 CYSWERLLR 1152

Search completed: February 21, 2003, 07:51:37
Job time : 5.2093 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
(without alignments)
114.078 Million cell updates/sec

Title: US-09-743-107b-90
Perfect score: 66
Sequence: 1 CFQWQXMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_invertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	89.4	711	4 Q8TCD2	Q8tcd2 homo sapien
2	55	83.3	38	4 Q9UCY5	Q9ucy5 homo sapien
3	50	75.8	33	6 Q9TR80	Q9tr80 ovis aries
4	41	62.1	105	10 Q9XFD5	Q9xfid5 oryza sativ
5	40	60.6	148	10 Q9XHP1	Q9xhp1 sesamum ind
6	40	60.6	275	5 Q93780	Q93780 caenorhabdi
7	40	60.6	932	5 Q19153	Q19153 caenorhabdi
8	39	59.1	205	16 Q986A0	Q986a0 rhizobium l
9	39	59.1	206	16 Q8UC62	Q8unc62 agrobacteri
10	39	59.1	206	16 Q92RH8	Q92rh8 rhizobium m
11	39	59.1	208	16 Q8VFK3	Q8vfk3 brucella me
12	39	59.1	279	16 Q8XSE2	Q8xse2 ralstonia s
13	39	59.1	306	4 Q8TAX2	Q8tax2 homo sapien
14	39	59.1	466	4 Q9NUS2	Q9nus2 homo sapien
15	38	57.6	91	15 Q77855	Q77855 human immun
16	38	57.6	91	15 Q77856	Q77856 human immun

Q96m2i homo sapien
Q96cn2 arabidopsis
Q22185 arabidopsis
Q22188 arabidopsis
Q9aws6 lycopersico
Q82536 salmonella
Q9yqcl human immun
Q9yqco human immun
Q9yqb9 human immun
Q9yqb8 human immun
Q9yji7 human immun
Q9yji2 human immun
Q94910 human immun
Q84454 human immun
Q8uek3 agrobacteri
Q44473 caenorhabdi
Q9nzw0 homo sapien
Q9nzw3 homo sapien
P96223 mycobacteri
Q9lhal arabidopsis
Q9hpa3 halobacteri
Q94937 homo sapien
Q62582 encephalito
Q8srg3 encephalito
Q8sg16 encephalito
Q9fhi9 arabidopsis
Q9imq5 lumpy skin
Q92cp0 oryza sativ

ALIGNMENTS

RESULT 1
Q8TCD2 PRELIMINARY; PRT; 711 AA.
ID Q8TCD2
AC Q8TCD2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Lactotraneferriin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347; AAH2347.1; -.
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 89.4%; Score 59; DB 4; Length 711;
Best Local Similarity 90.9%; Pred. No. 0.0067; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

Qy 1 CFQWQXMRKVR 11
| | | | |
Db 39 CFQWQXMRKVR 49

RESULT 2
Q9UCY5 PRELIMINARY; PRT; 38 AA.
ID Q9UCY5
AC Q9UCY5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Lactoferrin homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 RX (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96081613; PubMed=8551695;
 RT Sato I.;
 RA "Characterization of the 84-kDa protein with ABH activity in human
 RT seminal plasma";
 RL Jpn. J. Legal Med. 49:281-293(1995).
 DR HSP; P02788; IBKA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDEB CRC64;
 Query Match 83.3%; Score 55; DB 4; Length 38;
 Best Local Similarity 90.9%; Pred. No. 0.0019;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 FQWQKMKVR 12
 Db 21 FQWQKMKVR 31
 RESULT 3
 ID Q9TR80 PRELIMINARY; PRT; 33 AA.
 AC Q9TR80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE Lactoferrin (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=95127729; PubMed=7827104;
 RA Qian Z.Y., Jolles P., Migliore-Samou D., Fiat A.M.;
 RL Biochim. Biophys. Acta 1243:25-32(1995).
 DR HSP; O77698; ICE2
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
 Query Match 75.8%; Score 50; DB 6; Length 33;
 Best Local Similarity 63.6%; Pred. No. 0.014;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQWQKMKRV 11
 Db 19 CYWQKMKRL 29
 RESULT 4
 ID Q9XFD5 PRELIMINARY; PRT; 105 AA.
 AC Q9XFD5;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DE Cytochrome P450 (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=PANICLE;
 RA Liu J., Yang J.;
 RT "Suppression subtractive hybridization (SSH) identified candidate

RT genes that are differentially expressed at rice young panicle.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; AF140486; AAD29699.1; -.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR Pfam; PF00667; P450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
 KW Heme; Monooxygenase; Oxidoreductase.
 FT NON_TER 1
 SQ SEQUENCE 105 AA; 11912 MW; B0EEFCDD487E19F9 CRC64;
 Query Match 62.1%; Score 41; DB 10; Length 105;
 Best Local Similarity 60.0%; Pred. No. 2.3;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CFQWQKMKR 10
 Db 61 CFQWRLGKK 70
 RESULT 5
 ID Q9XHP1 PRELIMINARY; PRT; 148 AA.
 AC Q9XHP1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE 2S albumin.
 OS Sesamum indicum (Oriental sesame) (Gingelly).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
 OX NCBI_TaxID=4182;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=TAINAN 1;
 RX MEDLINE=20074970; PubMed=10606554;
 RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
 RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed
 RT storage proteins in sesame";
 RL J. Agric. Food Chem. 47:4932-4938(1999).
 DR EMBL; AF091841; AAD42943.1; -.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR000617; Napin.
 DR InterPro; IPR001768; Try/amy1 inhbr.
 DR Pfam; PF00234; try/alpha_aml; 1.
 DR PRINTS; PR00496; NAEIN.
 DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
 Query Match 60.6%; Score 40; DB 10; Length 148;
 Best Local Similarity 56.7%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQWQKMKR 9
 Db 54 CMQWMSMR 62
 RESULT 6
 ID Q93780 PRELIMINARY; PRT; 275 AA.
 AC Q93780;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P53H4.4 protein.
 GN P53H4.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Telodermata; Caenorhabditis.
 OX NCBI_TaxID=6239;

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IN  SEQUENCE FROM N.A.
RP  Dobson R.;
RL  Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
XX  MEDLINE=99069613; PubMed=9851916;
YA  none;
YT  "Genome sequence of the nematode C.elegans: A platform for
UT  investigating biology.";
YL  Science 282:2012-2018(1998).
XR  EMBL; Z81089; CAB03137.1; --
XQ  SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match          60.6%; Score 40; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 9.7;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Y  2 FQWQRMKVR 12
b  262 FQWKSMKTR 272
      |||: |||
      |||: |||

RESULT 7
19153 PRELIMINARY; PRT; 932 AA.
C  Q9153
D  Q19153;
T  01-NOV-1996 (TrEMBLrel. 01, Created)
T  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
T  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
E  Hypothetical 105.1 kDa protein.
F07C3.1.
S  Caenorhabditis elegans.
C  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
X  Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
P  SEQUENCE FROM N.A.
C  STRAIN=BRISTOL N2;
X  MEDLINE=99069613; PubMed=9851916;
A  None;
T  "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
[2]
P  SEQUENCE FROM N.A.
C  STRAIN=BRISTOL N2;
A  Faveillo A., Gattung S.;
T  "The sequence of C. elegans cosmid F07C3.";
Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
[3]
P  SEQUENCE FROM N.A.
C  STRAIN=BRISTOL N2;
A  Waterston R.;
T  "Direct Submission.";
L  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
R  EMBL; U50308; AAG24025.1; --
R  InterPro; IPR000731; HMGCR/patch_5TM.
R  PROSITE; PS50156; SSD; 1.
W  Hypothetical protein.
Q  SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;

Query Match          60.6%; Score 40; DB 5; Length 932;
Best Local Similarity 63.6%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Y  2 FQWQRMKVR 12
b  579 FQWQSRARLVK 589
      |||: |||
      |||: |||

RESULT 8
986A0 PRELIMINARY; PRT; 205 AA.
Q986A0 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Pyridoxamine 5'-phosphate oxidase.
GN  MLL7454.
OS  Rhizobium loti (Mesorhizobium loti).
OC  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC  Phyllobacteriaceae; Mesorhizobium.
OX  NCBI_TaxID=381;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=VAFF303099;
RX  MEDLINE=21082930; PubMed=11214968;
RA  Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA  Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA  Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA  Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA  Takeuchi C., Yamada M., Tabata S.;
RT  "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL  DNA Res. 7:331-338(2000).
DR  EMBL; AP003011; BAB53553.1; --
DR  InterPro; IPR000659; Pyridox oxidase.
DR  Pfam; PF01243; Pyridox oxidase; 1.
DR  ProDom; PD006312; Pyridox oxidase; 1.
DR  TIGRFAMs; TIGR00558; pdsH; 1.
DR  PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
KW  Complete proteome.
SQ  SEQUENCE 205 AA; 23300 MW; 0BADE4CD312327EA CRC64;

Query Match          59.1%; Score 39; DB 16; Length 205;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy  1 CFQWQRMKVR 12
Db  88 CFHWKSLRQVR 99
      |||: |||
      |||: |||

RESULT 9
Q8UHC2 PRELIMINARY; PRT; 206 AA.
ID  Q8UHC2
AC  Q8UHC2;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Pyridoxamine 5'-phosphate oxidase.
GN  PDXH OR ATU0760 OR AGR_C_1381.
OS  Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC  Rhizobiaceae; Rhizobium.
OX  NCBI_TaxID=176299;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21608550; PubMed=11743193;
RA  Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA  Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA  Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. Sr.,
RA  Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA  Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA  Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA  Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA  Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA  Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olsen M.V.,
RA  Nester E.W.;
RT  "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58.";
RL  Science 294:2317-2323(2001).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21608551; PubMed=11743194;

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RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Quorillo B., Gordon B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmlel K., Gordon J., Vaudin M., Iatchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Plangan C., Crowell C., Garson J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.,
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58,"
 RL Science 294:2323-2328(2001).
 DR EMBL: AE009043; AAL41776.1; -;
 DR EMBL: AE008009; AAK85569.1; -;
 KW Complete proteome.
 SQ SEQUENCE 206 AA; 23720 MW; 3BE48BAE5307C0C1 CRC64;

Query Match 59.1%; Score 39; DB 16; Length 206;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
 |||:|:|:
 Db 88 CFHWKSLRRQVR 99

RESULT 10

ID Q92RH8 PRELIMINARY; PRT; 206 AA.
 AC Q92RH8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Probable pyridoxamine 5'-phosphate oxidase (PNP/PMF oxidase) protein
 (EC 1.4.3.5).
 DE PDHX OR R00895 OR SMC00069.
 GN Rhizobium meliloti (Sinorhizobium meliloti).
 OS Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Rameperger U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021,"
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL: AL591785; CAC45467.1; -;
 DR InterPro; IPR000659; Pyridox oxidase.
 DR Pfam; PF01243; Pyridox oxidase; 1.
 DR ProDom; PD006312; Pyridox oxidase; 1.
 DR TIGRFAMs; TIGR00558; pdxH; 1.
 DR PROSITE; PS01064; PYRIDOX_OXIDASE; UNKNOWN_1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;

Query Match 59.1%; Score 39; DB 16; Length 206;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
 |||:|:|:
 Db 88 CFHWKSLRRQVR 99

RESULT 11

ID Q8YFK3 PRELIMINARY; PRT; 208 AA.
 AC Q8YFK3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

QY 1 CFQWQRMKVR 12
 |||:|:|:
 Db 88 CFHWKSLRRQVR 99

RESULT 12

ID Q8XSE2 PRELIMINARY; PRT; 279 AA.
 AC Q8XSE2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Putative ICC protein homolog.
 DE ICC OR RSP0534 OR RS00414.
 GN Ralstonia solanacearum (Pseudomonas solanacearum).
 OS Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choisme N., Claudel-Renard C., Cunha S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Siquier P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum,"
 RL Nature 415:497-502(2002).
 DR EMBL: AL646079; CAD17685.1; -;
 DR InterPro; IPR004843; M-ppetraxase.
 DR InterPro; IPR004844; S/T-phosphatase.
 DR Pfam; PF00149; Metallophos; 1.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 279 AA; 31541 MW; ABB39818004B2EDA CRC64;

Query Match 59.1%; Score 39; DB 16; Length 279;
 Best Local Similarity 41.7%; Pred. No. 15;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5).
 GN BME11517.
 OS Brucella melitensis
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA Delvechio V.G., Kapatral V., Redkar R.J., Patra G., Mujier C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Hasselkorn R., Kyprides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis,"
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL: AE009587; AAL52698.1; -;
 DR InterPro; IPR000659; Pyridox oxidase.
 DR Pfam; PF01243; Pyridox oxidase; 1.
 DR ProDom; PD006312; Pyridox oxidase; 1.
 DR TIGRFAMs; TIGR00558; pdxH; 1.
 DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 208 AA; 23866 MW; CBIF50BC9612DE28 CRC64;

Query Match 59.1%; Score 39; DB 16; Length 208;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
 |||:|:|:
 Db 90 CFHWKSLRRQVR 101

Query Match 59.1%; Score 39; DB 4; Length 466;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQXMR 9

DB 269 CFQWESTLR 277

RESULT 15

QY7855 PRELIMINARY; PRT; 91 AA.

AC Q77855;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Envelope protein (Fragment).
GN ENV.

OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95191002; PubMed=7884875;

RA Mulder-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J.,

RA Scherpbier H.J., de Perre P., Boer K., Goudsmit J.;

RT "Similarity in env and gag genes between genomic RNAs of human

RT immunodeficiency virus type 1 (HIV-1) from mother and infant is

RT unrelated to time of HIV-1 RNA positivity in the child.";

RL J. Virol. 69:2285-2296(1995).

DR EMBL; Z47867; CAA87881.1; -.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

KW AIDS; Coat protein; Glycoprotein.

FT NON TER 1 91

FT NON TER 1 91

SQ SEQUENCE 91 AA; 10530 MW; 8B10C62011F305D6 CRC64;

Query Match 57.6%; Score 38; DB 15; Length 91;
Best Local Similarity 60.0%; Pred. No. 7.4;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWQXMRKVR 12

DB 67 QWNETLQVR 76

Search completed: February 21, 2003, 08:00:44
Job time : 22.6744 secs

QY 1 CFQWQXMRKVR 12
DB 244 CFQWQXMRKVR 255

RESULT 13

QY7855 PRELIMINARY; PRT; 306 AA.

AC Q8TAX2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Similar to hypothetical protein FLJ11175.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX TISSUE=PANCREAS;

RA Strausberg R.;

RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC025708; AAH25708.1; -.

GW Hypothetical protein.

SQ SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;

Query Match 59.1%; Score 39; DB 4; Length 306;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQXMR 9

DB 269 CFQWESTLR 277

RESULT 14

QY7855 PRELIMINARY; PRT; 466 AA.

AC Q9NUS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE CDNA FLJ11175 fis, clone PLACE1007375, weakly similar to phorbol

DE ester/diacylglycerol-binding protein UNC-13.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX TISSUE=PLACENTA;

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Watanabe M., Hosoi T., Kodaira H., Kondo H., Sugawara M.,

RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuko Y.,

RA Ninomiya K., Iwayanagi T.;

RT "NEDO human cDNA sequencing project.";

RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK02037; BAA92048.1; -.

DR HSSP; P21707; 1BYN.

DR InterPro; IPR000008; C2.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF00169; C2; 1.

DR PRINTS; PR00360; C2DOMAIN.

DR SMART; SM00239; C2; 1.

DR PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.

DR PROSITE; PS50004; C2_DOMAIN_2; 1.

DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.

DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.

SQ SEQUENCE 466 AA; 53192 MW; E4113A5062F58D6E CRC64;

1	67	94.4	14	21	AAV78050	Human lactoferrin
2	12	94.4	14	21	AAV78051	Human lactoferrin
3	16	94.4	15	17	AAV78052	Peptide for anti-u
4	13	94.4	15	17	AAV98554	Human lactoferrin
5	14	94.4	15	21	AAV78053	Human lactoferrin
6	15	94.4	15	21	AAV78062	Human lactoferrin
7	67	94.4	15	21	AAV78063	Human lactoferrin
8	16	94.4	15	21	AAV78063	Human lactoferrin
9	17	94.4	16	21	AAV78031	Human lactoferrin
10	18	94.4	16	21	AAV78064	Human lactoferrin
11	17	94.4	16	21	AAV78064	Human lactoferrin
12	19	94.4	16	21	AAV78065	Human lactoferrin
13	20	94.4	16	21	AAV78034	Human lactoferrin
14	21	94.4	17	21	AAV78034	Human lactoferrin
15	22	94.4	17	21	AAV78066	Human lactoferrin
16	23	94.4	17	21	AAV78067	Human lactoferrin
17	24	94.4	18	15	AAV69352	Human lactoferrin
18	25	94.4	18	17	AAW13397	Advanced glycosyla
19	24	94.4	18	21	AAW13397	Human lactoferrin
20	26	94.4	19	21	AAV68867	Amino acid sequenc
21	27	94.4	19	21	AAV78032	Human lactoferrin
22	28	94.4	20	13	AAV21810	Anti microbial pep
23	29	94.4	20	14	AAV48481	Lactoferrin-relate
24	30	94.4	20	15	AAV48530	Lactoferrin derive
25	31	94.4	20	15	AAV48531	Lactoferrin derive
26	32	94.4	20	15	AAV57461	Lactoferrin derive
27	33	94.4	20	15	AAV57462	Lactoferrin derive
28	34	94.4	20	16	AAV84698	Bovine lactoferrin
29	35	94.4	20	16	AAV84698	Bovine lactoferrin
30	36	94.4	20	16	AAV84699	Bovine lactoferrin
31	37	94.4	20	16	AAV80263	Anti-parasitic lac
32	38	94.4	20	16	AAV80264	Anti-parasitic lac
33	39	94.4	20	17	AAV98553	Peptide for anti-u
34	40	94.4	20	17	AAV91852	Lactoferrin-derive
35	41	94.4	20	17	AAW03045	Lactoferrin-derive
36	42	94.4	20	17	AAV90607	Lactoferrin derive
37	43	94.4	20	17	AAV78621	Lactoferrin-derive
38	44	94.4	20	17	AAV78622	Lactoferrin-derive
39	45	94.4	20	18	AAW26150	Lactoferrin deriva
40	46	94.4	20	18	AAW14036	Anti-parasitic pep

RESULT 1

XX
AC AAY78091:

DT 25-APR-2000

Human lactoferrin derived peptide SEQ ID NO:91.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

de

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	71	100.0	12	21	AAV78091	Human lactoferrin
2	71	100.0	12	21	AAV78092	Human lactoferrin
3	67	94.4	12	21	AAV78038	Human lactoferrin
4	67	94.4	12	21	AAV78046	Human lactoferrin
5	67	94.4	12	21	AAV78047	Human lactoferrin
6	67	94.4	12	21	AAV78084	Human lactoferrin
7	67	94.4	13	21	AAV78037	Human lactoferrin
8	67	94.4	13	21	AAV78048	Human lactoferrin
9	67	94.4	13	21	AAV78049	Human lactoferrin
10	67	94.4	14	21	AAV78036	Human lactoferrin

XX PT New peptides used for treatment and prevention of infections, -
 XX PT Inflammations and tumors and for use in infant formula food -
 XX PS Claim 22; Page 38; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 100.0%; Score 71; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKNNMKVR 12
 DB 1 CFQWKNNMKVR 12
 |||||

RESULT 2
 AAY78092 ID AAY78092 standard; Peptide; 12 AA.
 AC AAY78092;
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:92.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections, -
 XX PT Inflammations and tumors and for use in infant formula food -
 XX PS Claim 22; Page 38; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 100.0%; Score 71; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKNNMKVR 12
 DB 1 CFQWKNNMKVR 12
 |||||

RESULT 3
 AAY78038 ID AAY78038 standard; Peptide; 12 AA.
 AC AAY78038;
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:38.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections, -
 XX PT Inflammations and tumors and for use in infant formula food -
 XX PS Claim 12; Page 70; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX Sequence 12 AA;

Query Match 94.4%; Score 67; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2y 1 CFQWKNRKRVR 12
|||:|||||
Db 1 CFQWKNRKRVR 12

RESULT 4

AY78046 ID AAY78046 standard; Peptide; 12 AA.

AY78046;

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:46.

Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.

Homo sapiens.

Synthetic.

WO200001730-A1.

13-JAN-2000.

06-JUL-1999; 99WO-SE01230.

06-JUL-1998; 98SE-0002441.

17-JUL-1998; 98SE-0002562.

29-DEC-1998; 98SE-0004614.

(ASCI-) A+ SCI INVEST AB.

Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections,
inflammations and tumors and for use in infant formula food -

Claim 15; Page 35; 102pp; English.

AY78001 to AAY78100 represent peptides having sequences based on human
lactoferrin. The peptides are taken up in the intestine through
binding to specific lactoferrin receptors and are then transported
through the circulation. A medicinal product of the peptide or fragment
can be used for treating and/or prevention of infections (such as
urinary tract infections, colitis, and Candida infection on a mucosal
membrane), inflammations and/or tumours. The peptides can also be used
in food stuffs such as infant formula food. The peptides are also
fungicidal and bactericidal and may also be used as preservatives.
Even though native human lactoferrin have been shown to have desired
anti-inflammatory anti-infectious and anti-tumoural properties they
cannot be used clinically on a broad basis because of high production
costs. Therefore, provision of peptides based on lactoferrin would
enable them to be used for the same purposes as lactoferrin at lower
cost.

XX Sequence 12 AA;
|||:|||||

Query Match 94.4%; Score 67; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNRKRVR 12
|||:|||||
Db 1 CFQWKNRKRVR 12

RESULT 5

AY78047 ID AAY78047 standard; Peptide; 12 AA.

AY78047;

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:47.

Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.

Homo sapiens.

Synthetic.

WO200001730-A1.

13-JAN-2000.

06-JUL-1999; 99WO-SE01230.

06-JUL-1998; 98SE-0002441.

17-JUL-1998; 98SE-0002562.

29-DEC-1998; 98SE-0004614.

(ASCI-) A+ SCI INVEST AB.

Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections,
inflammations and tumors and for use in infant formula food -

Claim 18; Page 73; 102pp; English.

AY78001 to AAY78100 represent peptides having sequences based on human
lactoferrin. The peptides are taken up in the intestine through
binding to specific lactoferrin receptors and are then transported
through the circulation. A medicinal product of the peptide or fragment
can be used for treating and/or prevention of infections (such as
urinary tract infections, colitis, and Candida infection on a mucosal
membrane), inflammations and/or tumours. The peptides can also be used
in food stuffs such as infant formula food. The peptides are also
fungicidal and bactericidal and may also be used as preservatives.
Even though native human lactoferrin have been shown to have desired
anti-inflammatory anti-infectious and anti-tumoural properties they
cannot be used clinically on a broad basis because of high production
costs. Therefore, provision of peptides based on lactoferrin would
enable them to be used for the same purposes as lactoferrin at lower
cost.

XX Sequence 12 AA;

Query Match 94.4%; Score 67; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWKNRMRKV 12
 DB 1 CFQWQNRMRKV 12

RESULT 6

AAV78084
 ID AAV78084 standard; Peptide; 12 AA.

AC AAV78084;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:84.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 22; Page 36; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;

Query Match 94.4%; Score 67; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 9.7e-05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWKNRMRKV 12
 DB 1 CFQWQNRMRKV 12

RESULT 7

AAV78037

ID AAV78037 standard; Peptide; 13 AA.

XX AAV78037;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 13 AA;

Query Match 94.4%; Score 67; DB 21; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.00011;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWKNRMRKV 12
 DB 2 CFQWQNRMRKV 13

RESULT 8

AAV78048
 ID AAV78048 standard; Peptide; 13 AA.

XX AAV78048;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:48.

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections, -
 PT inflammations and tumors and for use in infant formula food
 XX Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 14 AA;

Query Match 94.4%; Score 67; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00011;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNRMRKVR 12
 Db 3 CFQWQNRMRKVR 14

RESULT 11
 AAY78050
 ID AAY78050 standard; Peptide; 14 AA.

XX AAY78050;
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:50.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 XX 13-JAN-2000.

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections, -
 PT inflammations and tumors and for use in infant formula food
 XX Claim 15; Page 75; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 14 AA;

Query Match 94.4%; Score 67; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 0.00011;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNRMRKVR 12
 Db 3 CFQWQNRMRKVR 14

RESULT 12
 AAY78051
 ID AAY78051 standard; Peptide; 14 AA.

XX AAY78051;
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:51.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.

XX 13-JAN-2000.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections, -
 PT inflammations and tumors and for use in infant formula food
 XX

18 Claim 18; Page 75; 102pp; English.
 19 AAY78001 to AAY78100 represent peptides having sequences based on human
 20 lactoferrin. The peptides are taken up in the intestine through
 21 binding to specific lactoferrin receptors and are then transported
 22 through the circulation. A medicinal product of the peptide or fragment
 23 can be used for treating and/or prevention of infections (such as
 24 urinary tract infections, colitis, and Candida infection on a mucosal
 25 membrane), inflammations and/or tumours. The peptides can also be used
 26 in food stuffs such as infant formula food. The peptides are also
 27 fungicidal and bactericidal and may also be used as preservatives.
 28 Even though native human lactoferrin have been shown to have desired
 29 anti-inflammatory anti-infectious and anti-tumoural properties they
 30 cannot be used clinically on a broad basis because of high production
 31 costs. Therefore, provision of peptides based on lactoferrin would
 32 enable them to be used for the same purposes as lactoferrin at lower
 33 cost.
 34
 35 Query Sequence 14 AA;
 36 Query Match 94.4%; Score 67; DB 21; Length 14;
 37 Best Local Similarity 91.7%; Pred. No. 0.00011;
 38 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 39
 40 1 CFQWQRNRRKVR 12
 41 ||||:|||||
 42 3 CFQWQRNRRKVR 14
 43
 44 RESULT 13
 45 AAR98554
 46 AAR98554 standard; Peptide; 15 AA.
 47
 48 AAR98554;
 49
 50 12-NOV-1996 (first entry)
 51 Peptide for anti-ulcer agent.
 52
 53 anti-ulcer agent; low toxicity; stable; heat-resistant.
 54
 55 Synthetic.
 56
 57 JP08143468-A.
 58
 59 04-JUN-1996.
 60
 61 17-NOV-1994; 94JP-0283869.
 62
 63 17-NOV-1994; 94JP-0283869.
 64
 65 (MORG) MORINAGA MILK IND CO LTD.
 66
 67 WPI; 1996-318857/32.
 68
 69 Anti-ulcer agent contg. peptide - has low toxicity, is
 70 heat-resistant and water-soluble
 71
 72 Claim 1; Page 11; 11pp; Japanese.
 73
 74 AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
 75 in toxicity, is heat-resistant and stable in aqueous soln.. It can be
 76 administered orally and be produced in large amounts.
 77
 78 Query Sequence 15 AA;
 79 Query Match 94.4%; Score 67; DB 17; Length 15;
 80 Best Local Similarity 91.7%; Pred. No. 0.00012;
 81 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 82
 83 1 CFQWQRNRRKVR 12
 84 ||||:|||||
 85 2 CFQWQRNRRKVR 13

RESULT 14
 AAY78035
 ID AAY78035 standard; Peptide; 15 AA.
 XX
 AC AAY78035;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:35.
 XX
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX urinary tract infection; colitis; Candida infection; fungicidal;
 XX bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SE01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 XX
 PR 17-JUL-1998; 98SE-0002562.
 XX
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 12; Page 69; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 CC
 SQ Sequence 15 AA;
 Query Match 94.4%; Score 67; DB 21; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00012;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFQWQRNRRKVR 12
 ||||:|||||
 DB 4 CFQWQRNRRKVR 15
 RESULT 15
 AAY78062
 ID AAY78062 standard; Peptide; 15 AA.
 XX
 AC AAY78062;

XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:62.
DE
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
PN
XX 13-JAN-2000.
PD
XX 06-JUL-1999; 99WO-SE01230.
PF
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
DR
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
PT
XX
PS Claim 15; Page 81; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX
SQ Sequence 15 AA;
Query Match 94.4%; Score 67; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFQWXRNRKVR 12
| | | | |
Db 4 CFQWQRNRKVR 15

Search completed: February 21, 2003, 07:56:44
Job time : 29.093 secs

GenCore version 5.1.3
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DM protein - protein search, using sw model

Run on: February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds
(without alignments)
39.537 Million cell updates/sec

Title: US-09-743-107B-91
Perfect score: 71
Sequence: 1 CFQWRNMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PGTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	67	94.4	18	1	US-08-204-487-3 Sequence 3, Appl 1
2	67	94.4	18	2	US-08-485-948-8 Sequence 8, Appl 1
3	67	94.4	18	2	US-08-628-380-8 Sequence 8, Appl 1
4	67	94.4	18	2	US-08-475-055-8 Sequence 8, Appl 1
5	67	94.4	20	1	US-07-755-161A-3 Sequence 3, Appl 1
6	67	94.4	20	1	US-07-831-174-3 Sequence 3, Appl 1
7	67	94.4	20	1	US-08-204-487-1 Sequence 1, Appl 1
8	67	94.4	20	1	US-08-256-771-24 Sequence 24, Appl 1
9	67	94.4	20	1	US-08-256-771-25 Sequence 25, Appl 1
10	67	94.4	20	1	US-08-381-984-24 Sequence 24, Appl 1
11	67	94.4	20	1	US-08-381-984-25 Sequence 25, Appl 1
12	67	94.4	22	4	US-09-508-734-4 Sequence 4, Appl 1
13	67	94.4	24	4	US-09-508-734-6 Sequence 6, Appl 1
14	67	94.4	25	1	US-07-755-161A-10 Sequence 10, Appl 1
15	67	94.4	25	1	US-07-891-174-10 Sequence 10, Appl 1
16	67	94.4	25	1	US-08-204-487-7 Sequence 7, Appl 1
17	67	94.4	29	4	US-09-508-734-8 Sequence 8, Appl 1
18	67	94.4	36	1	US-07-755-161A-8 Sequence 8, Appl 1
19	67	94.4	36	1	US-07-891-174-8 Sequence 8, Appl 1
20	67	94.4	36	1	US-08-256-771-30 Sequence 30, Appl 1
21	67	94.4	36	1	US-08-381-984-29 Sequence 29, Appl 1
22	67	94.4	47	2	US-08-464-182A-6 Sequence 6, Appl 1
23	67	94.4	47	2	US-08-406-271-6 Sequence 6, Appl 1
24	67	94.4	50	2	US-08-693-274A-7 Sequence 7, Appl 1
25	67	94.4	52	4	US-09-017-043A-3 Sequence 3, Appl 1
26	67	94.4	53	2	US-08-464-182A-5 Sequence 5, Appl 1
27	67	94.4	53	2	US-08-406-271-5 Sequence 5, Appl 1

28	67	94.4	54	2	US-08-464-182A-2 Sequence 2, Appl 1
29	67	94.4	54	2	US-08-406-271-2 Sequence 2, Appl 1
30	67	94.4	634	3	US-08-724-586-2 Sequence 2, Appl 1
31	67	94.4	694	4	US-09-421-632-2 Sequence 2, Appl 1
32	67	94.4	694	4	US-09-932-190-2 Sequence 2, Appl 1
33	67	94.4	705	2	US-08-655-640-2 Sequence 2, Appl 1
34	67	94.4	708	2	US-08-655-640-4 Sequence 4, Appl 1
35	67	94.4	711	1	US-08-154-019-4 Sequence 4, Appl 1
36	67	94.4	711	1	US-08-461-333-4 Sequence 4, Appl 1
37	67	94.4	711	3	US-08-464-167-4 Sequence 4, Appl 1
38	67	94.4	711	3	US-09-158-313-4 Sequence 4, Appl 1
39	67	94.4	711	4	US-08-476-798-4 Sequence 2, Appl 1
40	64	90.1	711	1	US-08-145-681-2 Sequence 2, Appl 1
41	64	90.1	711	1	US-08-250-308-2 Sequence 2, Appl 1
42	64	90.1	711	1	US-08-453-703-2 Sequence 2, Appl 1
43	64	90.1	711	2	US-08-456-106-2 Sequence 2, Appl 1
44	64	90.1	711	3	US-08-456-108-2 Sequence 2, Appl 1
45	64	90.1	711	4	US-09-265-577-2 Sequence 2, Appl 1

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5563425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOIKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, KATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: RJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note="HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 94.4%; Score 67; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWGNRKVR 12
| | | | | | | | | |
Db 1 CFQWGNRKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/485,948
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-485-948-8

Query Match 94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWGNRKVR 12
| | | | | | | | | |
Db 1 CFQWGNRKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-628-380-8

Query Match 94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWGNRKVR 12
| | | | | | | | | |
Db 1 CFQWGNRKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475,055
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/485,948
;; FILING DATE:
;; APPLICATION NUMBER: 08/488,217
;; FILING DATE: JUNE 7, 1995
;; APPLICATION NUMBER: 08/418,642
;; FILING DATE: APRIL 7, 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 947-1-008A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; DESCRIPTION: LF-C1, 8-25
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; JS-08-475-055-8

Query Match 94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2y 1 CFQWKNNRKVR 12
2b 1 CFQWRNNRKVR 12

RESULT 5
JS-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible

;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: DisplayWrite
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/755,161A
;; FILING DATE: 19910905
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX: 202-371-8856
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 2
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 19"
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 19
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 2"
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
;; US-07-755-161A-3

Query Match 94.4%; Score 67; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 0.00011; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNMRKVR 12
||||:|||||

Db 2 CFQWQNRKVR 13

RESULT 6
US-07-891-174-3
Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNMRKVR 12
||||:|||||

Db 2 CFQWQNRKVR 13

RESULT 7
US-08-204-487-1
Sequence 1, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: DOSAKO, SHUN-ICHI
APPLICANT: KAWASAKI, YOSHITIRO
APPLICANT: UCHIDA, TOSHIKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESS: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: EJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1-20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNNRKVR 12
| | | | |
Db 2 CFQWRNNRKVR 13

RESULT 8
US-08-256-771-24
; Sequence 24, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
disulfide bond"

US-08-256-771-24

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNNRKVR 12
| | | | |
Db 2 CFQWRNNRKVR 13

RESULT 9
US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
prevent disulfide bond"

US-08-256-771-25

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNNRKVR 12
| | | | |
Db 2 CFQWRNNRKVR 13

RESULT 10
US-08-381-984-24

; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; US-08-381-984-24
Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFQWRNMRKVR 12
DB 2 CFQWRNMRKVR 13
RESULT 11
US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; US-08-381-984-25
Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFQWRNMRKVR 12
DB 2 CFQWRNMRKVR 13
RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: useful microorganism thereof
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; PRIOR APPLICATION NUMBER: PCI/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4

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/ LENGTH: 22
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-508-734-4
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Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKNRKVR 12
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Db 2 CFQWKNRKVR 13

RESULT 13
US-09-508-734-6
/ Sequence 6, Application US/09508734
/ Patent No. 6423509
/ GENERAL INFORMATION:
/ APPLICANT: Samyang Genex Corporation
/ TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
/ FILE REFERENCE: PA/SYG/00139
/ CURRENT APPLICATION NUMBER: US/09/508,734
/ PRIOR FILING DATE: 2000-06-01
/ PRIOR APPLICATION NUMBER: PCT/KR99/00373
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: KR1998-29351
/ PRIOR FILING DATE: 1998-07-13
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: Kopatentin 1.71
/ SEQ ID NO 6
/ LENGTH: 24
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-508-734-6

Query Match          94.4%; Score 67; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKNRKVR 12
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Db 3 CFQWKNRKVR 14

RESULT 14
US-07-755-161A-10
/ Sequence 10, Application US/07755161A
/ Patent No. 5304833
/ GENERAL INFORMATION:
/ APPLICANT: Mamoru TOMITA et al.
/ TITLE OF INVENTION: Antimicrobial Peptides and an
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wenderoth, Lind & Ponack
/ STREET: 805 Fifteenth Street, N.W., #700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: DisplayWrite
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/755,161A
/ FILING DATE: 19910905
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
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/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warren M. Cheek Jr.
/ REGISTRATION NUMBER: 33,367
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-8850
/ TELEFAX: 202-371-8856
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 amino acids
/ TYPE: AMINO ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE:
/ HYPOTHETICAL:
/ ANTI-SENSE:
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM:
/ STRAIN:
/ INDIVIDUAL ISOLATE:
/ DEVELOPMENTAL STAGE:
/ HAPLOTYPE:
/ TISSUE TYPE:
/ CELL TYPE:
/ CELL LINE:
/ ORGANELLE:
/ IMMEDIATE SOURCE:
/ LIBRARY:
/ CLONE:
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT:
/ MAP POSITION:
/ UNITS:
/ FEATURE:
/ NAME/KEY: modified site
/ LOCATION: 4
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: /note= "thiol group of
/ OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
/ OTHER INFORMATION: thiol group of Cys residue at location 21"
/ FEATURE:
/ NAME/KEY: modified site
/ LOCATION: 21
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: /note= "thiol group of
/ OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
/ OTHER INFORMATION: thiol group of Cys residue at location 4"
/ PUBLICATION INFORMATION:
/ AUTHORS:
/ TITLE:
/ JOURNAL:
/ VOLUME:
/ ISSUE:
/ PAGES:
/ DATE:
/ DOCUMENT NUMBER:
/ FILING DATE:
/ PUBLICATION DATE:
/ RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10

Query Match          94.4%; Score 67; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKNRKVR 12
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Db 4 CFQWKNRKVR 15
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RESULT 15

US-07-891-174-10
; Sequence 10 Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-891-174-10
; Query Match 94.4%; Score 67; DB 1; Length 25;
; Best Local Similarity 91.7%; Pred. No. 0.00013;
; Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 CFQWKGNNRKVR 12
; Db 4 CFQWKGNNRKVR 15
; Search completed: February 21, 2003, 08:04:26
; Job time : 8.93023 secs

GenCore version 5.1.3
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XM protein - protein search, using sw model

run on: February 21, 2003, 08:08:15 ; Search time 6.88372 Seconds
(without alignments)
54.162 Million cell updates/sec

Title: US-09-743-107B-91

Perfect score: 71

Sequence: 1 CFQWKNRMRKV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/prodata/2/pubpaa/PCF_NEW PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW PUB.pep.*
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- 14: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	94.4	15	9	US-09-798-869-2
2	67	94.4	25	9	US-09-798-869-20
3	67	94.4	694	9	US-10-023-096-2
4	59	83.1	15	9	US-09-798-869-6
5	50	70.4	15	9	US-09-798-869-3
6	50	70.4	25	9	US-09-798-869-23
7	42	59.2	15	9	US-09-798-869-7
8	41	57.7	15	9	US-09-798-869-4
9	41	57.7	25	9	US-09-798-869-22
10	39	54.9	333	9	US-09-796-753-26
11	38	53.5	15	9	US-09-798-869-8
12	38	53.5	15	9	US-09-798-869-29
13	38	53.5	15	9	US-09-798-869-30
14	38	53.5	21	10	US-09-864-761-47985
15	38	53.5	489	9	US-09-888-320-2
16	37	52.1	77	10	US-09-864-761-41002
17	37	52.1	86	9	US-09-738-626-5715
18	37	52.1	184	10	US-09-925-301-1248
19	37	52.1	338	9	US-09-978-295A-119

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20 37 52.1 338 9 US-09-978-697-119 Sequence 119, App
21 37 52.1 338 9 US-09-978-192A-119 Sequence 119, App
22 37 52.1 338 9 US-09-999-832A-119 Sequence 119, App
23 37 52.1 338 9 US-09-978-189-119 Sequence 119, App
24 37 52.1 553 9 US-09-796-753-14 Sequence 14, Appl
25 37 52.1 553 10 US-09-981-649A-6 Sequence 6, Appl
26 37 52.1 553 10 US-09-981-649A-24 Sequence 24, Appl
27 37 52.1 554 10 US-09-981-649A-30 Sequence 30, Appl
28 37 52.1 554 10 US-09-981-649A-32 Sequence 32, Appl
29 37 52.1 559 10 US-09-981-649A-28 Sequence 28, Appl
30 35 49.3 301 9 US-10-080-960-11 Sequence 11, Appl
31 35 49.3 302 10 US-09-948-078-2 Sequence 2, Appl
32 35 49.3 351 10 US-09-853-625B-16 Sequence 16, Appl
33 35 49.3 1013 9 US-10-028-072-38 Sequence 38, Appl
34 35 49.3 1013 9 US-10-121-043-38 Sequence 38, Appl
35 35 49.3 1013 9 US-10-123-904-38 Sequence 38, Appl
36 35 49.3 1013 9 US-10-140-470-38 Sequence 38, Appl
37 35 49.3 1013 9 US-10-175-746-38 Sequence 38, Appl
38 35 49.3 1013 9 US-10-176-918-38 Sequence 38, Appl
39 35 49.3 1013 9 US-10-176-921-38 Sequence 38, Appl
40 35 49.3 1013 9 US-10-137-865-38 Sequence 38, Appl
41 35 49.3 1013 9 US-10-140-474-38 Sequence 38, Appl
42 34 47.9 62 10 US-09-815-242-12129 Sequence 12129, A
43 34 47.9 62 10 US-09-815-242-13026 Sequence 13026, A
44 34 47.9 509 10 US-09-879-957-194 Sequence 194, App
45 34 47.9 846 9 US-10-051-409-4 Sequence 4, Appl

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ALIGNMENTS

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RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049.PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

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Query Match 94.4%; Score 67; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 5.1e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CFQWKNRMRKV 12
Db 3 CFQWKNRMRKV 14

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RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON

```

APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/G899/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match 94.4%; Score 67; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 8.2e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKNNMKVR 12
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Db 3 CFQWQNNMKVR 14

RESULT 3
US-10-023-096-2
Sequence 2, Application US/10023096
Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25.
CURRENT APPLICATION DATA:
FILING DATE: US/10/023,096
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-023-096-2

Query Match 94.4%; Score 67; DB 9; Length 694;
Best Local Similarity 91.7%; Pred. No. 0.0017;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKNNMKVR 12
|||:|||||
Db 22 CFQWQNNMKVR 33

RESULT 4
US-09-798-869-6
Sequence 6, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/G899/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match 83.1%; Score 59; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.001;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKNNMKVR 12
|||:|||||
Db 3 CFQWQNNMKVR 14

RESULT 5
US-09-798-869-3
Sequence 3, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/G899/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: CAPRINE
US-09-798-869-3

Query Match 70.4%; Score 50; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.028;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKNRKV 11
|:|:|:|:
DB 3 CYQWQRMKRL 13

RESULT 6

US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 70.4%; Score 50; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.045;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKNRKV 11
|:|:|:|:
DB 3 CYQWQRMKRL 13

RESULT 7

US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 59.2%; Score 42; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.55;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKNRKV 11
|:|:|:|:
DB 3 CYQWQRMKRL 13

RESULT 8

US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 57.7%; Score 41; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.8;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNRKV 11
|:|:|:|:
DB 3 CLRQWQRMKRV 13

RESULT 9

US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 57.7%; Score 41; DB 9; Length 25;
Best Local Similarity 54.5%; Pred. No. 1.3;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNRKV 11
|:|:|:|:
DB 3 CLRQWQRMKRV 13

RESULT 10

US-09-796-753-26
; Sequence 26, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 26
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Mouse
US-09-796-753-26

Query Match 54.9%; Score 39; DB 9; Length 333;
Best Local Similarity 54.5%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNMRKV 11
|:|:|:|:|:
Db 48 CYGWRNKGV 58

RESULT 11

US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US2003002821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8

Query Match 53.5%; Score 38; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 2.4;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNMRKV 11
|:|:|:|:|:
Db 3 CLRQWEMRKV 13

RESULT 12

US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US2003002821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 53.5%; Score 38; DB 9; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.4;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKNMRKV 11
|:|:|:|:|:
Db 3 CLRQWEMRKV 13

Db 3 CFWQWRMKKL 13

RESULT 13

JS-09-798-869-30
; Sequence 30, Application US/09798869
; Publication No. US2003002282A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
JS-09-798-869-30

Query Match 53.5%; Score 38; DB 9; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.4;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Y 1 CFWQWRMKKV 11

Db 3 CFWQWRMKKL 13

RESULT 14

JS-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47985
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL096701.14
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUE 1.00e-06
US-09-864-761-47985

Query Match 53.5%; Score 38; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1 CFWQKR 6

Db 16 CFWQKR 21

RESULT 15

US-09-888-320-2
; Sequence 2, Application US/09888320
; Publication No. US20030013090A1
; GENERAL INFORMATION:
; APPLICANT: Barry III, Clifton E.
; APPLICANT: DeBarber, Andrea E.
; APPLICANT: Mdulili, Khisimuzi
; APPLICANT: Bekker, Linda-Gail
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
; FILE REFERENCE: 015280-413100US
; CURRENT APPLICATION NUMBER: US/09/888,320
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/214,187
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-888-320-2

Query Match 53.5%; Score 38; DB 9; Length 489;
Best Local Similarity 54.5%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Y 1 CFWQWRMKKV 11

Db 253 CFWQWRMKKM 263

Search completed: February 21, 2003, 08:11:56
Job time : 6.88372 secs

GenCore version 5.1.3
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DM protein - protein search, using sw model

Run on: February 21, 2003, 07:48:01 ; Search time 10.6047 Seconds
(without alignments)
108.784 Million cell updates/sec

Title: US-09-743-107B-91

Perfect score: 71

Sequence: 1 CFQWKRNRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	67	94.4	711	1	TPHUL	Lactotransferrin p
2	50	70.4	708	2	JC2323	Lactoferrin - goat
3	47	66.2	33	2	S52107	Lactoferrin - sheep
4	45	63.4	275	2	T22597	Hypothetical prote
5	41	57.7	206	2	H97451	Pyridoxamine 5',-ph
6	41	57.7	206	2	AB2670	Probable pyridoxam
7	41	57.7	208	2	AC3441	Hypothetical prote
8	41	57.7	511	2	AB0858	Lactoferrin precu
9	41	57.7	707	1	A28438	Hypothetical prote
10	40	56.3	584	2	C84325	Dynamin beta heavy
11	40	56.3	4568	2	T08030	Hypothetical prote
12	39	54.9	447	2	T18633	Hypothetical prote
13	39	54.9	759	2	G86506	Hypothetical prote
14	39	54.9	759	2	G72115	Hypothetical prote
15	38	53.5	60	2	A48396	Ribosomal protein
16	38	53.5	62	2	AH1301	Ribosomal protein
17	38	53.5	267	2	AH1673	Ribosomal protein
18	38	53.5	267	2	S77802	Hypothetical prote
19	38	53.5	298	2	AD2346	Hypothetical prote
20	38	53.5	393	2	B64639	3-Deoxy-manno-octu
21	38	53.5	489	2	C70655	Probable monooxyge
22	38	53.5	583	2	T01470	Diphosphate-fructo
23	37	52.1	205	2	E90094	26S proteasome SU
24	37	52.1	214	2	S07989	Vif protein - simi
25	37	52.1	274	2	B60950	Apolipoprotein B-1
26	37	52.1	357	2	T22879	Hypothetical prote
27	37	52.1	513	2	E86156	Ti4P4.7 protein -
28	37	52.1	518	2	B4514	Probable cytochrom
29	37	52.1	536	2	T24218	Hypothetical prote

hypothetical prote
GTP-binding regula
hypothetical prote
trichosyalin like
hypothetical prote
hypothetical prote
F1511.22 [imported
hypothetical prote
60S ribosomal prot
hypothetical prote
hypothetical prote
pre-pilin leader p
33.3K hypothetical
hypothetical prote
hypothetical prote
MHC class I histoc
pectate lyase (EC

ALIGNMENTS

RESULT 1

TPHUL

Lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence, revision 21-Nov-1997 #text change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S7

R/Cho, Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DDBT

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R/Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148,'T',150-422,'C',424-711 <REY>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactofe

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A/Experimental source: Placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogdren, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <STI>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28,'X',30-31 <ST2>

F;359-696/Domain:	transferrin repeat homology <TRH2>	F;252,300,387,495,564/Binding site:	carbohydrate (Asn)	(covalent)	#status predicted
-------------------	------------------------------------	-------------------------------------	--------------------	------------	-------------------

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BME11517

A;Map position: I

C;Superfamily: pyridoxamine-phosphate oxidase

C;Keywords: oxidoreductase

Query Match 57.7%; Score 41; DB 2; Length 208;

Best Local Similarity 58.3%; Pred. No. 8.3;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKRMKVR 12

DB 90 CFHWKSLRQVR 101

RESULT 8

AB0858

hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Typh

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C;Accession: AB0858

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; PMID:11677608

A;Accession: AB0858

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-511 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:gl6504016; GSPDB:GNC00176

C;Genetics:

A;Gene: STY3070

Query Match 57.7%; Score 41; DB 2; Length 511;

Best Local Similarity 58.3%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWKRMKVR 12

DB 350 CFWDNMKAKVR 361

RESULT 9

A28438

lactoferrin precursor - mouse

N;Alternate names: lactotransferrin

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A28438; A41205

R;Pentecost, B.T.; Teng, C.T.

J. Biol. Chem. 262, 10134-10139, 1987

A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret

A;Reference number: A92596; MUID:87280033; PMID:3611056

A;Accession: A28438

A;Molecule type: mRNA

A;Residues: 3-707 <PEN>

A;Cross-references: EMBL:J03298

R;Liu, Y.; Teng, C.T.

J. Biol. Chem. 266, 21880-21885, 1991

A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.

A;Reference number: A41205; MUID:92042099; PMID:1939212

A;Accession: A41205

A;Molecule type: DNA

A;Residues: 1-15 <LTU>

A;Cross-references: GB:M74778

C;Superfamily: transferrin; transferrin repeat homology

C;Keywords: duplication; glycoprotein

P;1-19/Domain: signal sequence #status predicted <SIG>

F;20-707/Product: lactotransferrin #status predicted <MAT>
 F;358-595/Domain: transferrin repeat homology <TRH>
 F;494/Binding site: carbonydrate (Asn) (covalent) #status predicted

Query Match 57.7%; Score 41; DB 1; Length 707;
 Best Local Similarity 54.5%; Pred. No. 28;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNRKRKV 11
 |||:|:|:|

Db 37 CLRQWNRKRKV 47

RESULT 10

C84325
 hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1
 C;Species: Halobacterium sp. NRC-1
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C;Accession: C84325
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
 ; Leitthausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabil
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504483; PMID:11016950
 A;Accession: C84325
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-584 <STO>
 A;Cross-references: GB:AE004437; NID:g10581192; PIDN:AAI19967.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: VNG1732C

Query Match 56.3%; Score 40; DB 2; Length 584;
 Best Local Similarity 41.7%; Pred. No. 34;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNRKRKV 12
 |||:|:|:|

Db 445 CFTWRKDMRKRKV 456

RESULT 11

T08030
 dynein beta heavy chain - Chlamydomonas reinhardtii
 C;Species: Chlamydomonas reinhardtii
 C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
 C;Accession: T08030
 R;Mitchell, D.R.; Brown, K.S.
 J. Cell Sci. 107, 635-644, 1994
 A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
 A;Reference number: Z18302; MUID:194274778; PMID:8006077
 A;Accession: T08030
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-4568 <MIT>
 A;Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
 A;Experimental source: strain 21gr
 C;Genetics:
 A;Gene: ODA4

A;Map position: IX
 A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
 3334/3; 3686/3; 3892/3; 4240/3
 C;Superfamily: dynein heavy chain, ciliary
 C;Keywords: nucleotide binding; P-loop
 F;1919-1926/Region: nucleotide-binding motif A (P-loop)
 F;2202-2209/Region: nucleotide-binding motif A (P-loop)
 F;2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 56.3%; Score 40; DB 2; Length 4568;
 Best Local Similarity 41.7%; Pred. No. 2.6e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNRKRKV 12
 |||:|:|:|

Db 1852 CFQWSQLRYIQ 1863

RESULT 12

T18633
 hypothetical protein M18.8 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T18633; T23799
 R;Sims, M.
 submitted to the EMBL Data Library, February 1996
 A;Reference number: Z18999
 A;Accession: T18633
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-447 <WIL>
 A;Cross-references: EMBL:Z69634; PIDN:CAA93457.1; GSPDB:GN00022; CESP:M18.8
 A;Experimental source: clone B0001
 R;Steward, C.
 submitted to the EMBL Data Library, January 1996
 A;Reference number: Z19800
 A;Accession: T23799
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-447 <W12>
 A;Cross-references: EMBL:Z68507; PIDN:CAA92831.1; GSPDB:GN00022; CESP:M18.8
 A;Experimental source: clone M18
 C;Genetics:
 A;Gene: CESP:M18.8
 A;Map position: 4
 A;Introns: 41/3; 137/1; 326/3; 434/2

Query Match 54.9%; Score 39; DB 2; Length 447;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 WKENMRKV 11
 |||:|:|:|

Db 291 WKENLRV 298

RESULT 13

G86506
 hypothetical protein CFJ0126 [imported] - Chlamydomonas pneumoniae (strain J138)
 C;Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C;Accession: G86506
 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
 Nucleic Acids Res. 28, 2311-2314, 2000
 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A;Reference number: A86491; MUID:20330349; PMID:10871362
 A;Accession: G86506
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-759 <STO>
 A;Cross-references: GB:BA000008; NID:g9978500; PIDN:BAA98337.1; GSPDB:GN00142
 A;Experimental source: strain J138
 C;Genetics:
 A;Gene: CFJ0126

Query Match 54.9%; Score 39; DB 2; Length 759;
 Best Local Similarity 66.7%; Pred. No. 66;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWKNRKRKV 11
 |||:|:|:|

Db 488 QWKNLRDV 496

RESULT 14

72115
 ypothetical protein CP0646 [imported] - Chlamydia pneumoniae (strains CWL029 and AR
 ;Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 ;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 ;Accession: G72115, F81554
 ;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 ature Genet. 21, 385-389, 1999
 ;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 ;Reference number: A72000; MUID:99206606; PMID:10192388
 ;Accession: G72115
 ;Status: preliminary
 ;Molecule type: DNA
 ;Residues: 1-759 <ARN>
 ;Cross-references: GB:AE001599; GB:AE001363; NID:94376387; PIDN:AAD18279.1; PID:9437639
 ;Experimental source: strain CWL029
 ;Read, T.D.; Brunkham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwin, M.; Nelson, M.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 ;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 ;Reference number: A81500; MUID:20150255; PMID:10684935
 ;Accession: F81554
 ;Status: preliminary
 ;Molecule type: DNA
 ;Residues: 1-759 <REA>
 ;Cross-references: GB:AE002222; GB:AE002161; NID:97189553; PIDN:AAF38461.1; PID:9718956
 ;Experimental source: strain AR39, HL cells
 ;Genetics:
 ;Gene: CP0126; CP0646

Query Match 54.9%; Score 39; DB 2; Length 759;
 Best Local Similarity 66.7%; Pred. No. 66;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

2y 3 QWKNMKV 11
 |||:|:|
 2b 488 QWKNLRDV 496

RESULT 15
 A48396
 ribosomal protein L28 - Bacillus stearothermophilus
 C:Species: Bacillus stearothermophilus
 C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 21-Aug-1998
 C:Accession: A48396
 R;Kruft, V.; Kapp, U.; Wittmann-Liebold, B.
 Biochimie 73, 855-860, 1991
 A;Title: Characterization and primary structure of proteins L28, L33 and L34 from Bacill
 A;Reference number: A48396; MUID:92075758; PMID:1742360
 A;Accession: A48396
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-60 <KKU>
 A;Note: sequence extracted from NCBI backbone (NCBIP:69662)
 C;Superfamily: Escherichia coli ribosomal protein L28

Query Match 53.5%; Score 38; DB 2; Length 60;
 Best Local Similarity 66.7%; Pred. No. 8.2;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WKNMKVR 12
 |||:|:|
 Db 27 WKANLQVR 35

Search completed: February 21, 2003, 08:02:46
 Job time : 11.6047 secs

GenCore version 5.1.3
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DM protein - protein search, using sw model

Run on: February 21, 2003, 07:28:06 ; Search time 5.2093 Seconds
 (without alignments)
 95.544 Million cell updates/sec

Title: US-09-743-107B-91
 Perfect score: 71
 Sequence: 1 CFQKKNRKVR 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	67	94.4	711	1 TRFL_HUMAN	P02788 homo sapien
2	50	70.4	708	1 TRFL_CAMDR	Q92400 camelus dro
3	50	70.4	708	1 TRFL_CAPHI	Q29477 capra hircu
4	42	59.2	695	1 TRFL_HORSE	Q07811 equus cabal
5	41	57.7	62	1 RL28_THETN	Q8r9u1 thermomanae
6	41	57.7	707	1 TRFL_MOUSE	P08071 mus musculu
7	40	56.3	4568	1 DYHB_CHLRE	Q39565 chlamydomon
8	39	54.9	292	1 NLA_DROME	Q9x218 drosophila
9	38	53.5	60	1 RL28_BACST	P23374 bacillus st
10	38	53.5	62	1 RL28_LISMO	Q924j2 listeria mo
11	38	53.5	146	1 RPOB_LIBAF	P41187 liberibacte
12	38	53.5	267	1 Y125_MYCCA	P53661 mycoplasma
13	37	52.1	214	1 VIF_SIVS4	P12505 simian immu
14	37	52.1	783	1 YNR2_CAEEL	Q21988 caenorhabdi
15	36	50.7	365	1 IAX3_HUMAN	P30453 homo sapien
16	36	50.7	455	1 YKYL_CAEEL	Q19910 caenorhabdi
17	36	50.7	485	1 GLGA_BACST	Q08328 bacillus st
18	36	50.7	502	1 C932_SOYBN	Q42799 glycine max
19	36	50.7	509	1 C931_SOYBN	Q42798 glycine max
20	36	50.7	510	1 C933_SOYBN	Q81973 glycine max
21	36	50.7	528	1 CAX2_ARATH	Q38798 arabidopsis
22	36	50.7	530	1 CAX3_ARATH	P29402 arabidopsis
23	36	50.7	728	1 KDGI_ARATH	Q39017 arabidopsis
24	36	50.7	749	1 VP4_ROTGA	Q04916 rotavirus (
25	36	50.7	1135	1 PHYC_SORBI	Q93528 sorghum bic
26	35	49.3	151	1 SYB2_RHIME	Q923q1 rhizobium m
27	35	49.3	215	1 VIF_HV2SB	P12452 human immun
28	35	49.3	215	1 VIF_HV2ST	P20878 human immun
29	35	49.3	343	1 SP2D_BACSU	F07372 bacillus su
30	35	49.3	344	1 SP2D_BACAM	P13251 bacillus am
31	35	49.3	351	1 NOV_CHICK	P28686 gallus gall
32	35	49.3	358	1 DDL_ENTHR	Q47827 enterococcu
33	35	49.3	398	1 YK13_CAEEL	P34337 caenorhabdi

ALIGNMENTS

RESULT 1

ID	TRFL_HUMAN	STANDARD	PRT:	711 AA
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H1Z3; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C].			
GN	LIF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Connely O.M.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RL	"Molecular cloning and sequence analysis of human lactoferrin.";			
RT	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Radu T.A.;			
RL	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RT	sequences.";			
RL	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RL	"cDNA cloning and sequence analysis of human lactoferrin.";			
RT	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

Q9vfn2 drosophila
 Q9bjj9 chlamydia m
 Q9ute7 schizosacch
 P35649 eikenella c
 P58306 thermoplasma
 Q9ulc6 homo sapien
 Q99up4 staphylococ
 P29328 ovis aries
 Q10353 schizosacch
 P43488 mus musculu
 P19506 simian immu
 Q55185 synechocyst

RA SEQUENCE OF 3-711 FROM N.A.
 RC TISSUE-Mammary Gland;
 RX MEDLINE=90326549; PubMed=2374734;
 RA Powell M.J., Ogden J.E.;
 RT "Nucleotide sequence of human lactoferrin cDNA.";
 RL Nucleic Acids Res. 18:4013-4013(1990).
 RN [9]
 RP SEQUENCE OF 20-711.
 RX MEDLINE=85076667; PubMed=6510420;
 RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
 RT Metz-Boutigue M.-H., Jolles J., Jolles P.;
 RL "Human lactotransferrin: amino acid sequence and structural
 RT comparisons with other transferrins.";
 RL Eur. J. Biochem. 145:659-666(1984).
 RN [10]
 RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
 RX MEDLINE=82046817; PubMed=6794640;
 RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
 RT Jolles P.;
 RL "The present state of the human lactotransferrin sequence. Study and
 RT alignment of the cyanogen bromide fragments and characterization of
 RT N- and C-terminal domains.";
 RL Biochim. Biophys. Acta 670:243-254(1981).
 RN [11]
 RP SEQUENCE OF 609-711.
 RX MEDLINE=82262043; PubMed=7049727;
 RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
 RT Jolles P.;
 RL "An 88 amino acid long C-terminal sequence of human
 RT lactotransferrin.";
 RL FEBS Lett. 142:107-110(1982).
 RN [12]
 RP SEQUENCE OF 436-711 FROM N.A.
 RX MEDLINE=88001031; PubMed=3477300;
 RA Rado T.A., Wei X., Benz E.J. Jr.;
 RT "Isolation of lactoferrin cDNA from a human myeloid library and
 RT expression of mRNA during normal and leukemic myelopoiesis.";
 RL Blood 70:989-993(1987).
 RN [13]
 RP SEQUENCE OF 237-711 FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
 RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
 RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
 RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
 RA Sagripanti J.L.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
 RX MEDLINE=90064528; PubMed=2585506;
 RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
 RT "Structure of human lactoferrin: crystallographic structure analysis
 RT and refinement at 2.8-A resolution.";
 RL J. Mol. Biol. 209:711-734(1989).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RA Haridas M., Anderson B.F., Baker E.N.;
 RT "Structure of human diferric lactoferrin refined at 2.2-A
 RT resolution.";
 RL Acta Crystallogr. D 51:629-646(1995).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
 RX MEDLINE=97156796; PubMed=9003186;
 RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
 RA Baker E.N.;
 RT "Matogenesis of the histidine ligand in human lactoferrin: iron
 RT binding properties and crystal structure of the histidine-
 RT 253-->methionine mutant.";
 RL Biochemistry 36:341-346(1997).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=99190892; PubMed=10089347;
 RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
 RT "Structure of recombinant human lactoferrin expressed in Aspergillus
 RL Acta Crystallogr. D 55:403-407(1999).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=99192677; PubMed=10089508;
 RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
 RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
 RT and analysis of ligand-induced conformational change.";
 RL Acta Crystallogr. D 54:1319-1335(1998).
 RN [19]
 RP CHARACTERIZATION OF LACTOFERROXINS.
 RX MEDLINE=911166929; PubMed=1369293;
 RA Tani F., Iio K., Chiba H., Yoshikawa M.;
 RT "Isolation and characterization of opioid antagonist peptides derived
 RT from human lactoferrin.";
 RL Agric. Biol. Chem. 54:1803-1810(1990).
 RN [20]
 RP VARIANTS THR-30 AND ARG-48.
 RX PubMed=9873069;
 RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
 RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
 RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
 RA El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
 RA Hejtmancik J.F., Teng C.T.;
 RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
 RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
 RL Mol. Vision 4:31-32(1998).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
 CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
 CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
 CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 CC
 DR EMBL; X53961; CAA37914.1; -
 DR EMBL; U07643; AAB60324.1; -
 DR EMBL; X93150; AAA36159.1; -
 DR EMBL; M83202; AAA59811.1; -
 DR EMBL; M83205; AAA58656.1; -
 DR EMBL; M18642; AAA86665.1; -
 DR EMBL; AF332168; AAG48753.1; -
 DR EMBL; BC015822; AAH15822.1; -
 DR EMBL; BC015823; AAH15823.1; -
 DR EMBL; W73700; AAA59479.1; -
 DR EMBL; X52941; CAA37116.1; -
 DR EMBL; U95626; AAB57795.1; -
 DR PIR; S11228; TFHUL.
 DR PDB; 1LCF; 31-AUG-94.
 DR PDB; 1LCT; 31-OCT-93.
 DR PDB; 1LFG; 31-JUL-94.
 DR PDB; 1LFH; 31-OCT-93.
 DR PDB; 1LFI; 31-OCT-93.
 DR PDB; 1LGB; 31-AUG-94.
 DR PDB; 1LGC; 31-AUG-94.
 DR PDB; 1BKA; 08-NOV-96.
 DR PDB; 1DSN; 08-MAR-96.
 DR PDB; 1HSE; 12-MAR-97.
 DR PDB; 1VFD; 21-APR-97.

Query Match 94.4%; Score 67; DB 1; Length 711;
 Best Local Similarity 91.7%; Pred. No. 0.0002;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKENMKVR 12
 DB 39 CFQWQNRMKVR 50

RESULT 2
 TRFL CAMDR STANDARD; PRT; 708 AA.
 AC Q9TUM0: Q9MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabic camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Somali; TISSUE=Lactating mammary gland;
 RA Kappler S.R., Ackermann M., Farah Z., Puhon Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
 RL Int. Dairy J. 9:481-486 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 CC -----

DR EMBL; AJ131674; CAB53387.1; -;
 DR EMBL; AF165879; AAF82241.1; -;
 DR HSSP; O77811; 1B1X.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin.2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2;
 DR PROSITE; PS00206; TRANSFERRIN_2; 2;
 DR PROSITE; PS00207; TRANSFERRIN_3; 2;
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT SIGNAL. 1 19 BY SIMILARITY.
 FT CHAIN 20 708 LACTOTRANSFERRIN.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.
 FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 ANION (BY SIMILARITY).
 FT BINDING 482 482 ANION (BY SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 261 261 F -> S (IN REF. 2).
 FT CONFLICT 304 304 G -> A (IN REF. 2).
 FT CONFLICT 330 330 S -> P (IN REF. 2).
 FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
 FT CONFLICT 506 506 L -> F (IN REF. 2).
 FT CONFLICT 609 609 A -> P (IN REF. 2).
 FT CONFLICT 642 642 R -> Q (IN REF. 2).
 SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 70.4%; Score 50; DB 1; Length 708;
 Best Local Similarity 66.7%; Pred. No. 0.22;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNRMKVR 12
 DB 38 CAQWQNRMKVR 49

RESULT 3
 TRFL CAPHI STANDARD; PRT; 708 AA.
 ID TRFL CAPHI
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=94380047; PubMed=8093048;
 RA le Provost F., Nocart M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 RT relevant locus to bovine U12 syntenic group.";
 RL Biochem. Biophys. Res. Commun. 203:1324-1332 (1994).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.


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FT DISULFID 453 538
FT DISULFID 487 681
FT DISULFID 497 511
FT DISULFID 508 521
FT DISULFID 579 593
FT DISULFID 631 636
FT METAL 56 66
FT METAL 98 98
FT METAL 198 198
FT METAL 259 259
FT METAL 401 401
FT METAL 439 439
FT METAL 532 532
FT METAL 601 601
FT BINDING 127 127
FT BINDING 469 469
FT CARBOHYD 143 143
FT CARBOHYD 287 287
FT CARBOHYD 482 482
SQ SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 59.2%; Score 42; DB 1; Length 695;
Best Local Similarity 58.3%; Pred. No. 5.7;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

2y 1 CFQWKNNRKVR 12
   :|||:|
Db 25 CAKFQNNKVR 36

RESULT 5
RL28 THETN STANDARD; PRT; 62 AA.
AC Q8R9U1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 50S ribosomal protein L28.
EN RPMB OR TTE1495.
OS Thermoaerobacter tengcongensis.
CC Bacteria; Firmicutes; Clostridia; Thermoaerobacteriales;
CC Thermoaerobacteriaceae; Thermoaerobacter.
CX NCBI_taxid=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
CC -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
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DR EMBL; AE013107; AM24713.1; -
DR Ribosomal protein; Complete proteome.
GW SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
SQ SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;

Query Match 57.7%; Score 41; DB 1; Length 62;
Best Local Similarity 70.0%; Pred. No. 0.69;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

2y 3 QKNNRKVR 12
   :|||:|
2b 27 RWKNNRKVR 36

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RESULT 6
TRFL_MOUSE
ID TRFL_MOUSE STANDARD; PRT; 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RC MEDLINE=87280033; PubMed=3611056;
RX Pentecost B.T., Teng C.T.;
RA "Lactotransferrin is the major estrogen inducible protein of mouse
RA uterine secretions.";
RL J. Biol. Chem. 262:10134-10139(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Morishima K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=92042099; PubMed=1939212;
RA Liu Y., Teng C.T.;
RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21895(1991).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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DR EMBL; J03298; AAA40525.1; -
DR EMBL; D88510; BAA13633.1; -
DR EMBL; BC006904; AAH06904.1; -
DR EMBL; M74778; AAA39427.1; -
DR PIR; A28438; A28438.
DR HSP; P02788; ICB6.
DR MGD; MGI:96837; Ltf.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal.
FT CHAIN 1 19 BY SIMILARITY.
FT CHAIN 20 707 LACTOTRANSFERRIN.
FT REPEAT 20 357 1.

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FT REPEAT 358 707 2.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.
FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 263 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 423 702 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 78 IRON 1 (BY SIMILARITY).
FT METAL 110 110 IRON 1 (BY SIMILARITY).
FT METAL 210 210 IRON 1 (BY SIMILARITY).
FT METAL 271 271 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 451 451 IRON 2 (BY SIMILARITY).
FT METAL 544 544 IRON 2 (BY SIMILARITY).
FT METAL 613 613 IRON 2 (BY SIMILARITY).
FT BINDING 139 139 ANION (POTENTIAL).
FT BINDING 481 481 ANION (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLUCNA. .) (POTENTIAL).
FT CARBOHYD 494 494 MR -> IOG (IN REF. 1).
FT CONFLICT 1 2 R -> Q (IN REF. 2).
FT CONFLICT 25 25 M -> L (IN REF. 2).
FT CONFLICT 82 82 A -> T (IN REF. 2).
FT CONFLICT 359 359 A -> D (IN REF. 1).
FT CONFLICT 382 382 E -> G (IN REF. 2).
FT CONFLICT 449 449 L -> V (IN REF. 1).
FT CONFLICT 629 629
SQ SEQUENCE 707 AA; 77865 MW, F26AE03404C19A8 CRC64;

Query Match 57.7%; Score 41; DB 1; Length 707;
Best Local Similarity 54.5%; Pred. No. 8.7;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNMKRV 11
DB 37 CLRQWENMKV 47

RESULT 7
DYHB CHLRE
ID DYHB CHLRE STANDARD; PRT; 4568 AA.
AC Q3955;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
CX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21GI;
RC MEDLINE=94274778; PubMed=8006077;
RA Mitchell D.R., Brown K.S.;
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
chain genes";
RL J. Cell Sci. 107:635-644 (1994).
CC -1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
CC FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -1- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
CC GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.

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CC -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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CC
CC EMBL; U02963; AAA19956.1; -.
CC InterPro; IPR004273; Dynein heavy.
CC Pfam; PF03028; Dynein heavy; 1.
CC Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
KW Coiled coil.
FT DOMAIN 277 293 COILED COIL (POTENTIAL).
FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
FT NP_BIND 1919 1926 ATP (POTENTIAL).
FT NP_BIND 2202 2209 ATP (POTENTIAL).
FT NP_BIND 2530 2537 ATP (POTENTIAL).
FT NP_BIND 2879 2886 ATP (POTENTIAL).
SQ SEQUENCE 4568 AA; 519961 MW, 9A9A5393C7C36AE7 CRC64;

Query Match 56.3%; Score 40; DB 1; Length 4568;
Best Local Similarity 41.7%; Pred. No. 92;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNMKRV 12
DB 1852 CFQWQSLRYIQ 1863

RESULT 8
NLA DROME
ID NLA DROME STANDARD; PRT; 292 AA.
AC Q9XZL8; Q9V391;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nebula protein.
GN NLA OR CG6072.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA McCormick A.V., Goldberg M.L.;
RT "Gene required for elongation of meiosis I spindle in Drosophila
females.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Branton R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos F.V., Berman B.P., Bhandari D., Bolshakov S.,

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DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
DR AIDS.
SQ SEQUENCE 214 AA; 25140 MW; 9BCE884EC454BF3D CRC64;
Query Match 52.1%; Score 37; DB 1; Length 214;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;
2y 3 QWKRNRK 10
2b 170 QWRNRK 177
RESULT 14
YNR2_CABEL STANDARD; PRT; 783 AA.
AC Q21988;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein R13G10.2 in chromosome III.
3N R13G10.2.
3S Caenorhabditis elegans.
3C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
3X Rhabditidae; Peloderinae; Caenorhabditis.
3N NCBI_TaxID=6239;
3N [1]
SEQUENCE FROM N.A.
3C STRAIN=Bristol N2;
3A Gardner A.E.;
3L Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
3N [2]
3C REVISIONS.
3A Durbin R.;
3L Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
3C -!- COPACTOR: FAD (POTENTIAL).
3C -!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
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3C or send an email to license@isb-sib.ch).
3C -----
3C EMBL; Z35602; CA84671.2; -
3C Wormpep; R13G10.2; CE25088.
3C InterPro; IPR002937; Amino oxidase.
3C Pfam; PF01593; Amino_oxidase; 1.
3C Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
3C NP_BIND 311 366 FAD (ADP PART) (POTENTIAL).
3C SEQUENCE 783 AA; 88799 MW; 8D087E96464DC908 CRC64;
Query Match 52.1%; Score 37; DB 1; Length 783;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
2y 1 CFQWKRNRKVR 12
2b 540 CIDWGRDRKVR 551
RESULT 15
LA34_HUMAN STANDARD; PRT; 365 AA.
3C P30453; P20454;
3C 01-APR-1993 (Rel. 25, Created)
3C 01-APR-1993 (Rel. 25, Last sequence update)
3C 16-OCT-2001 (Rel. 40, Last annotation update)
3C HLA class I histocompatibility antigen, AW-34(A-10) alpha chain
DE HLA-A OR HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
SEQUENCE FROM N.A. (A*3401/A*3402).
MEDLINE=93056508; PubMed=1491115;
RA Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
RA Martell R.W., du Toit E.D., Parham P.;
RA "Distinctive HLA-A,B antigens of black populations formed by
RA interallelic conversion.";
RA J. Immunol. 149:3411-3415(1992).
RN [2]
SEQUENCE FROM N.A. (A*3401/A*3402).
MEDLINE=93235211; PubMed=8475492;
RA Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
RA du Toit E.D., Parham P.;
RA "Structural diversity in the HLA-A10 family of alleles: correlations
RA with serology.";
RA Tissue Antigens 41:72-80(1993).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401
CC (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
CC A*3401.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X61704; CAA3873.1; -
CC EMBL; X61705; CAA3874.1; -
CC PIR; S16767; S16767.
CC PIR; S16771; S16771.
CC HSP; O19673; IHSB.
CC MIM; 142800.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003597; IG_cl.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00047; IG; 1.
CC ProDom; PD000050; MHC_I; 1.
CC SMART; SM00407; IGcl; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT SIGNAL 25 365
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT AW-34(A-10) ALPHA CHAIN.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT CYTOPLASMIC TAIL.
FT N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT I -> V (IN A*3402).
FT /FTID=VAR_004379.
FT K -> N (IN A*3402).
FT /FTID=VAR_004380.
FT R -> I (IN A*3402).
FT /FTID=VAR_004381.
FT VARIANT 121 121
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FT VARIANT 129 129 P -> S (IN A*3402).
FT VARIANT 138 138 /FTid=VAR 004382.
FT VARIANT 180 180 Q -> R (IN A*3402).
FT VARIANT 180 180 /FTid=VAR 004383.
FT VARIANT 312 312 W -> L (IN A*3402).
FT VARIANT 312 312 /FTid=VAR 004384.
FT VARIANT 312 312 L -> I (IN A*3402).
FT VARIANT 312 312 /FTid=VAR 004385.
SQ SEQUENCE 365 AA; 41055 MW; 063BF63E68E01F6 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 365;
Best Local Similarity 66.7%; Pred. NO. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 4 WKRNRKVR 12
Db 84 WDRNRKVK 92

```

Search completed: February 21, 2003, 07:51:38
Job time : 6.2093 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
(without alignments)
114.078 Million cell updates/sec

Title: US-09-743-107B-91

Perfect score: 71

Sequence: 1 CFQWKNRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_mycobacteri:*
- 9: sp_mycobacteri:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rviro:*
- 16: sp_bacteriopl:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	62	87.3	711	4 Q8TCD2	Q8tcd2 homo sapien
2	58	81.7	38	4 Q9UCY5	Q9ucy5 homo sapien
3	47	66.2	33	6 Q9TR80	Q9tr80 ovis aries
4	45	63.4	275	5 Q93780	Q93780 caenorhabdi
5	41	57.7	62	16 Q8E9U1	Q8e9ul thermococci
6	41	57.7	205	16 Q986A0	Q986a0 rhizobium l
7	41	57.7	206	16 Q8UHC2	Q8uhc2 agrobacteri
8	41	57.7	208	16 Q92RH8	Q92rh8 rhizobium m
9	41	57.7	208	16 Q8YFK3	Q8yfk3 brucella me
10	41	57.7	511	16 Q82462	Q82462 salmonella
11	40	56.3	81	15 Q90863	Q90863 human immun
12	40	56.3	148	10 Q9XHP1	Q9xhpi sesamum ind
13	40	56.3	274	4 Q96M21	Q96m21 homo sapien
14	40	56.3	584	17 Q9HPA3	Q9hpa3 halobacteri
15	39	54.9	273	2 Q31090	Q31090 rhizobium l
16	39	54.9	279	16 Q8XSE2	Q8kse2 ralstonia s

17	39	54.9	447	5	017549	017549 caenorhabdi
18	39	54.9	550	11	Q9JUZ5	Q9juz5 mus musculu
19	39	54.9	759	16	Q92955	Q92955 chlamydia p
20	39	54.9	864	5	O62582	O62582 encephalito
21	39	54.9	864	5	Q8SRG3	Q8srg3 encephalito
22	39	54.9	864	5	Q8SQI6	Q8sqi6 encephalito
23	38	53.5	81	15	Q90884	Q90884 human immun
24	38	53.5	91	15	Q77855	Q77855 human immun
25	38	53.5	105	10	Q9XFD5	Q9xfds oryza sativ
26	38	53.5	207	10	Q9SML1	Q9sml1 cicer ariet
27	38	53.5	240	10	Q9SML2	Q9sml2 cicer ariet
28	38	53.5	253	12	Q68541	Q68541 horseradish
29	38	53.5	298	16	Q8YP77	Q8yp77 anabaena sp
30	38	53.5	306	4	Q8TAX2	Q8tax2 homo sapien
31	38	53.5	329	2	Q9F7Y4	Q9f7y4 salmonella
32	38	53.5	341	11	Q8R2A4	Q8r2a4 mus musculu
33	38	53.5	372	10	O81653	O81653 hemerocalli
34	38	53.5	393	10	Q92TP0	Q92tp0 oryza sativ
35	38	53.5	393	16	O25611	O25611 helicobacte
36	38	53.5	402	10	Q92RH8	Q92rh8 oryza sativ
37	38	53.5	466	4	Q9NUS2	Q9nus2 homo sapien
38	38	53.5	489	16	P96223	P96223 mycobacteri
39	38	53.5	499	10	Q9XFX1	Q9xfx1 cicer ariet
40	38	53.5	560	10	Q9FTT0	Q9ftt0 oryza sativ
41	38	53.5	570	10	O89487	O89487 zea mays (m
42	38	53.5	583	10	O81437	O81437 arabidopsis
43	38	53.5	662	12	Q9QU30	Q9qu30 ttv-like mi
44	38	53.5	666	5	Q9WIDS	Q9wid5 drosophila
45	38	53.5	866	10	Q9FHI9	Q9fhi9 arabidopsis

ALIGNMENTS

RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2; 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC022347; AAH22347.1; --
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 87.3%; Score 62; DB 4; Length 711;
Best Local Similarity 90.9%; Pred. No. 0.0074;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNRKVR 11
Db 39 CFQWKNRKVR 49

RESULT 2

Q9UCY5 PRELIMINARY; PRT; 38 AA.
ID Q9UCY5
AC Q9UCY5; 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE Lactoferrin homolog (fragment)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96081613; PubMed=8551695;
 RA Sato I.;
 RT "Characterization of the 84-kDa protein with ABH activity in human
 RT seminal plasma.";
 RL Jpn. J. Legal Med. 49:281-293(1995).
 DR HSSP; P02788; IBAK.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDDB CRC64;

Query Match 81.7%; Score 58; DB 4; Length 38;
 Best Local Similarity 90.9%; Pred. No. 0.0019;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWKNMRKVR 12
 |||:|||||
 Db 21 FQWKNMRKVR 31

RESULT 3
 Q9TR80 PRELIMINARY; PRT; 33 AA.
 AC Q9TR80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95127729; PubMed=7827104;
 RA Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
 RL Biochim. Biophys. Acta 1243:25-32(1995).
 DR HSSP; O77698; 1CE2.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 66.2%; Score 47; DB 6; Length 33;
 Best Local Similarity 54.5%; Pred. No. 0.16;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKNMRKV 11
 |:|:|:|:|:
 Db 19 CYQWQKNMRKL 29

RESULT 4
 Q93780 PRELIMINARY; PRT; 275 AA.
 AC Q93780;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE F53H4.4 protein.
 GN F53H4.4
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dobson R.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z81089; CAB03137.1; -;
 SQ SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 63.4%; Score 45; DB 5; Length 275;
 Best Local Similarity 72.7%; Pred. No. 3.1;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWKNMRKVR 12
 |||:|||||
 Db 262 FQWKNMRKTR 272

RESULT 5
 Q8R9U1 PRELIMINARY; PRT; 62 AA.
 AC Q8R9U1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Ribosomal protein L28.
 GN RPMB OR TTE1495.
 OS Thermoaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Thermoaerobacteriales; Thermoaerobacteriaceae; Thermoaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4T / JCM11007;
 RX MEDLINE=21992816; PubMed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of T. tengcongensis genome.";
 RL Genome Res. 12:689-700(2002).
 DR EMBL; AE013107; AAM24713.1; -;
 KW Complete proteome.
 SQ SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;

Query Match 57.7%; Score 41; DB 16; Length 62;
 Best Local Similarity 70.0%; Pred. No. 3.6;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWKNMRKVR 12
 :|||:|:
 Db 27 RWKFNIRKVR 36

RESULT 6
 Q986A0 PRELIMINARY; PRT; 205 AA.
 AC Q986A0;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Pyridoxamine 5'-phosphate oxidase.
 GN ML17454.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Igesawa K., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP03011; BAB3553.1; -.
 DR InterPro; IPR000659; Pyridox oxidase.
 DR Pfam; PF01243; Pyridox oxidase; 1.
 DR ProDom; PD06312; Pyridox oxidase; 1.
 DR TIGRfam; TIGR00558; pdxH; 1.
 DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
 KW Complete proteome.
 SQ SEQUENCE 205 AA; 23300 MW; 0BADE4CD312327EA CRC64;

Query Match 57.7%; Score 41; DB 16; Length 205;

Best Local Similarity 58.3%; Pred. No. 12; Mismatches 4; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKNNRQVR 12
 |||||
 DB 88 CFHWKSLRRQVR 99

RESULT 7

ID Q8UHC2 PRELIMINARY; PRT; 206 AA.
 AC Q8UHC2;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Pyridoxamine 5'-phosphate oxidase.
 EN PDHX OR ATU0760 OR AGR C 1381.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 CX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.I., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutyavina T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphumachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58.";
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Gorman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmieu K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursion J., Lono C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 DR EMBL; AE009043; AAL41776.1; -.
 DR EMBL; AE008009; AAK86569.1; -.
 KW Complete proteome.
 SQ SEQUENCE 206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;

Query Match 57.7%; Score 41; DB 16; Length 206;

Best Local Similarity 58.3%; Pred. No. 12; Mismatches 4; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKNNRQVR 12
 |||||
 DB 88 CFHWKSLRRQVR 99

QY 1 CFQWKNNRQVR 12
 |||||
 DB 88 CFHWKSLRRQVR 99

RESULT 8

ID Q92RH8 PRELIMINARY; PRT; 206 AA.
 AC Q92RH8;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Probable pyridoxamine 5'-phosphate oxidase (PNP/EMP oxidase) protein
 DE (EC 1.4.3.5).
 EN PDHX OR R00895 OR SMC00069.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 CX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godrie T., Goffeau D., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetle D., Puehler A., Fumelle B., Ramsperger U.,
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL; AL591785; CAC45467.1; -.
 DR InterPro; IPR000659; Pyridox oxidase.
 DR Pfam; PF01243; Pyridox oxidase; 1.
 DR ProDom; PD06312; Pyridox oxidase; 1.
 DR TIGRfam; TIGR00558; pdxH; 1.
 DR PROSITE; PS01064; PYRIDOX_OXIDASE; UNKNOWN 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;

Query Match 57.7%; Score 41; DB 16; Length 206;

Best Local Similarity 58.3%; Pred. No. 12; Mismatches 4; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKNNRQVR 12
 |||||
 DB 88 CFHWKSLRRQVR 99

RESULT 9

ID Q8YFK3 PRELIMINARY; PRT; 208 AA.
 AC Q8YFK3;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5).
 GN BME1157.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 CX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujar C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyripides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.";

```

Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
DR EMBL; AE009597; AAL52498.1; -.
DR InterPro; IPR000659; Pyridox_Oxidase.
DR Pfam; PF01243; Pyridox_oxidase; 1.
DR ProDom; PD006312; Pyridox_oxidase; 1.
DR TIGRFAMs; TIGR00558; pdxH; 1.
DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
DR OXIDOREDUCTASE; Complete proteome.
SQ SEQUENCE 208 AA; 23866 MW; CB1F50BC9612DE28 CRC64;

Query Match 57.7%; Score 41; DB 16; Length 208;
Best Local Similarity 58.3%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKNRNVKVR 12
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DB 90 CFHWKSLRRQVR 101

RESULT 10
ID O82462 PRELIMINARY; PRT; 511 AA.
AC O82462;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein STY3070.
GN STY3070.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davies P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar typhi CT18."
RL Nature 413:848-852 (2001).
DR EMBL; AL627276; CAD06049.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 511 AA; 59126 MW; E2DDDD124E10D178B CRC64;

Query Match 57.7%; Score 41; DB 16; Length 511;
Best Local Similarity 58.3%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWKNRNVKVR 12
||| |||
DB 350 CFADWDMNKAQVR 361

RESULT 11
ID O90863 PRELIMINARY; PRT; 81 AA.
AC O90863;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein gp120 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=NUS182;
RA Brandful J.A.M., Ampofo W.K., Janssens W., Adu-Sarkodie Y.,
RA Apegyei F., Anyomi F., Aidoo S., Barnor J.S., Yamamoto N.,
RA Ishikawa K., Sata T., Kurata T.;
RT "Genetic and phylogenetic analysis of HIV-1 strains from Southern
RT Ghana."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225659; CAA12541.1; -.
DR InterPro; IPR000777; GPI20.
DR Pfam; PF00516; GPI20; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9138 MW; 2D43DCD554295572 CRC64;

Query Match 56.3%; Score 40; DB 15; Length 81;
Best Local Similarity 66.7%; Pred. No. 7.1;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWKNRMKRV 11
||| |||
DB 69 EWKENLRKV 77

RESULT 12
ID Q9XHP1 PRELIMINARY; PRT; 148 AA.
AC Q9XHP1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TAINAN 1;
RX MEDLINE=20074970; PubMed=10606554;
RA Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
RT "Molecular cloning of 11S globulin and 2S albumin, the two major seed
RT storage proteins in sesame."
RL J. Agric. Food Chem. 47:4932-4938 (1999).
DR EMBL; AF091841; AAD42943.1; -.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR003617; Napin.
DR InterPro; IPR001768; Try/amyI_inhbr.
DR Pfam; PF00234; tryp_alpha_ami1; 1.
DR PRINTS; PR00496; NAFIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 56.3%; Score 40; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKNRNV 9
||| |||
DB 54 CMQWMSMR 62

RESULT 13
ID Q96M21 PRELIMINARY; PRT; 274 AA.
AC Q96M21;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CDNA FLJ32891 fis, clone TESTI2004929.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
 RA Arita M., Mutsaers K., Yuuki H., Hara H., Sugiyama T., Irie R.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanohori K., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK057453; BAB71433.1; -;
 SQ SEQUENCE 274 AA; 30083 MW; 1DD43654D4135B2F CRC64;

Query Match 56.3%; Score 40; DB 4; Length 274;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

2Y 1 CFQWKNMKVR 12
 |||:|:|:|:
 3b 66 CFQWGVGYRLR 77

RESULT 14
 29HPA3 PRELIMINARY; PRT; 584 AA.
 ID Q9HPA3
 AC Q9HPA3
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Vng1732c.
 EN Vng1732c.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 CC Halobacteriaceae; Halobacterium.
 DX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsen V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angewine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Fohlstroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1";
 UL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE005078; AAG19967.1; -;
 DR InterPro; IPR001646; 5peptide repeat.
 DR InterPro; IPR001622; K+channel_pore.
 DR Pfam; PF00805; Pentapeptide; 2.
 KW Complete proteome.
 SQ SEQUENCE 584 AA; 65151 MW; 21BF5D5F0486CCC6 CRC64;

Query Match 56.3%; Score 40; DB 17; Length 584;
 Best Local Similarity 41.7%; Pred. No. 54;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

2Y 1 CFQWKNMKVR 12
 |||:|:|:|:
 3b 445 CFQWGVGYRLR 456

RESULT 15
 231090 PRELIMINARY; PRT; 273 AA.
 ID O31090
 AC O31090;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Hypothetical 31.0 kDa protein.
 OS Rhizobium leguminosarum (biovar viciae).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=387;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF39;
 RA Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF39;
 RX MEDLINE=99113394; PubMed=9914965;
 RA Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G.,
 RA Ksenzenko V.N.;
 RT "Structural and functional organization of the exopolysaccharide
 biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39";
 RL Mol. Biol. (Mosk) 32:797-804(1998).
 DR EMBL; AF028810; AAB88891.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;

Query Match 54.9%; Score 39; DB 2; Length 273;
 Best Local Similarity 60.0%; Pred. No. 37;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWKNMKVR 12
 :|:|:|:|:
 Db 245 RWLNLRKLR 254

Search completed: February 21, 2003, 08:00.44
 Job time : 21.6744 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:37:21 ; Search time 28.093 Seconds
(without alignments)
56.918 Million cell updates/sec

Title: US-09-743-107B-92

Perfect score: 71

Sequence: 1 CFQWKENMKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID32/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	71	100.0	12	21 AAY78091	Human lactoferrin
2	71	100.0	12	21 AAY78092	Human lactoferrin
3	67	94.4	12	21 AAY78038	Human lactoferrin
4	67	94.4	12	21 AAY78045	Human lactoferrin
5	67	94.4	12	21 AAY78047	Human lactoferrin
6	67	94.4	12	21 AAY78084	Human lactoferrin
7	67	94.4	13	21 AAY78037	Human lactoferrin
8	67	94.4	13	21 AAY78048	Human lactoferrin
9	67	94.4	13	21 AAY78049	Human lactoferrin
10	67	94.4	14	21 AAY78036	Human lactoferrin

11	67	94.4	14	21	AAY78050	Human lactoferrin
12	67	94.4	14	21	AAY78051	Human lactoferrin
13	67	94.4	15	17	AA998554	Peptide for anti-u
14	67	94.4	15	21	AAY78035	Human lactoferrin
15	67	94.4	15	21	AAY78062	Human lactoferrin
16	67	94.4	15	21	AAY78063	Human lactoferrin
17	67	94.4	16	21	AAY78031	Human lactoferrin
18	67	94.4	16	21	AAY78064	Human lactoferrin
19	67	94.4	16	21	AAY78065	Human lactoferrin
20	67	94.4	17	21	AAY78034	Human lactoferrin
21	67	94.4	17	21	AAY78066	Human lactoferrin
22	67	94.4	17	21	AAY78067	Human lactoferrin
23	67	94.4	18	15	AA995352	Human lactoferrin
24	67	94.4	18	17	AAW13397	Advanced glycosyla
25	67	94.4	18	21	AAY78033	Human lactoferrin
26	67	94.4	19	21	AAY68867	Amino acid sequenc
27	67	94.4	19	21	AAY78032	Human lactoferrin
28	67	94.4	20	13	AA921810	Anti microbial pep
29	67	94.4	20	14	AA944841	Lactoferrin-relate
30	67	94.4	20	15	AA948530	Lactoferrin derive
31	67	94.4	20	15	AA948531	Lactoferrin derive
32	67	94.4	20	15	AA957461	Lactoferrin derive
33	67	94.4	20	15	AA957462	Lactoferrin derive
34	67	94.4	20	16	AA946698	Bovine lactoferrin
35	67	94.4	20	16	AA946699	Bovine lactoferrin
36	67	94.4	20	16	AA980263	Anti-parasitic lac
37	67	94.4	20	16	AA980264	Anti-parasitic lac
38	67	94.4	20	17	AA998553	Peptide for anti-u
39	67	94.4	20	17	AA991852	Lactoferrin-derive
40	67	94.4	20	17	AAW03045	Lactoferrin-derive
41	67	94.4	20	17	AA930607	Lactoferrin-derive
42	67	94.4	20	17	AA937621	Lactoferrin-derive
43	67	94.4	20	17	AA937622	Lactoferrin-derive
44	67	94.4	20	18	AAW26150	Lactoferrin deriva
45	67	94.4	20	18	AAW14036	Anti-parasitic pep

ALIGNMENTS

RESULT 1
AAY78091
ID AAY78091 standard; Peptide; 12 AA.
XX
AC AAY78091;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:91.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.

CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX SQ Sequence 12 AA;

Query Match 94.4%; Score 67; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNRKVR 12
| | | | | | | | | |
Db 1 CFQWRNRKVR 12

RESULT 4

AAV78046
ID AAY78046 standard; Peptide; 12 AA.

XX AC AAY78046;

XX 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:46.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.

XX OS Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections, -

XX inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX SQ Sequence 12 AA;

Query Match 94.4%; Score 67; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNRKVR 12
| | | | | | | | | |
Db 1 CFQWRNRKVR 12

RESULT 5

AAV78047
ID AAY78047 standard; Peptide; 12 AA.

XX AC AAY78047;

XX 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:47.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.

XX OS Homo sapiens.

OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections, -
XX inflammations and tumors and for use in infant formula food -

XX Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX SQ Sequence 12 AA;

Query Match 94.4%; Score 67; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKRNRKVR 12
 DB 1 CFQWKRNRKVR 12

RESULT 6

AAV78084
 ID AAV78084 standard; Peptide; 12 AA.

AC AAV78084;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:84.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCII-) A+ SCI INVEST AB.
 PA Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 22; Page 36; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Query Match 94.4%; Score 67; DB 21; Length 12;
 XX Best Local Similarity 91.7%; Pred. No. 9.7e-05;
 XX Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFQWKRNRKVR 12
 DB 1 CFQWKRNRKVR 12

RESULT 7

AAV78037

ID AAV78037 standard; Peptide; 13 AA.
 AC AAV78037;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:37.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200001730-A1.
 PN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 PF 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCII-) A+ SCI INVEST AB.
 PA Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 70; 102pp; English.

XX AAV78001 to AAV78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX Query Match 94.4%; Score 67; DB 21; Length 13;
 XX Best Local Similarity 91.7%; Pred. No. 0.00011;
 XX Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFQWKRNRKVR 12
 DB 2 CFQWKRNRKVR 13

RESULT 8

AAV78048
 ID AAV78048 standard; Peptide; 13 AA.
 AC AAV78048;
 XX 25-APR-2000 (first entry)
 DT Human lactoferrin derived peptide SEQ ID NO:48.
 DE Human lactoferrin derived peptide SEQ ID NO:48.

```
XX Human, lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200001730-A1.  
XX 13-JAN-2000.  
XX 06-JUL-1999; 99WO-S01230.  
XX 06-JUL-1998; 98SE-0002441.  
XX 17-JUL-1998; 98SE-0002562.  
XX 29-DEC-1998; 98SE-0004614.  
XX (ASCI-) A+ SCI INVEST AB.  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.  
XX New peptides used for treatment and prevention of infections,  
XX inflammations and tumors and for use in infant formula food  
XX Claim 15; Page 74; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human  
XX lactoferrin. The peptides are taken up in the intestine through  
XX binding to specific lactoferrin receptors and are then transported  
XX through the circulation. A medicinal product of the peptide or fragment  
XX can be used for treating and/or prevention of infections (such as  
XX urinary tract infections, colitis, and Candida infection on a mucosal  
XX membrane), inflammations and/or tumours. The peptides can also be used  
XX in food stuffs such as infant formula food. The peptides are also  
XX fungicidal and bactericidal and may also be used as preservatives.  
XX Even though native human lactoferrin have been shown to have desired  
XX anti-inflammatory anti-infectious and anti-tumoural properties they  
XX cannot be used clinically on a broad basis because of high production  
XX costs. Therefore, provision of peptides based on lactoferrin would  
XX enable them to be used for the same purposes as lactoferrin at lower  
XX cost.  
XX  
XX Sequence 13 AA;  
SQ  
Query Match 94.4%; Score 67; DB 21; Length 13;  
Best Local Similarity 91.7%; Pred. No. 0.00011;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CFQWQNRNKRVR 12  
Db 2 CFQWQNRNKRVR 13  
RESULT 9  
AAY78049  
ID AAY78049 standard; Peptide; 13 AA.  
XX  
XX AAY78049;  
XX  
XX 25-APR-2000 (first entry)  
DT Human lactoferrin derived peptide SEQ ID NO:49.  
XX  
XX  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
XX Homo sapiens.  
OS
```

```
OS Synthetic.  
XX WO200001730-A1.  
XX 13-JAN-2000.  
XX 06-JUL-1999; 99WO-S01230.  
XX 06-JUL-1998; 98SE-0002441.  
XX 17-JUL-1998; 98SE-0002562.  
XX 29-DEC-1998; 98SE-0004614.  
XX (ASCI-) A+ SCI INVEST AB.  
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;  
XX WPI; 2000-147388/13.  
XX New peptides used for treatment and prevention of infections,  
XX inflammations and tumors and for use in infant formula food  
XX Claim 18; Page 74; 102pp; English.  
XX  
XX AAY78001 to AAY78100 represent peptides having sequences based on human  
XX lactoferrin. The peptides are taken up in the intestine through  
XX binding to specific lactoferrin receptors and are then transported  
XX through the circulation. A medicinal product of the peptide or fragment  
XX can be used for treating and/or prevention of infections (such as  
XX urinary tract infections, colitis, and Candida infection on a mucosal  
XX membrane), inflammations and/or tumours. The peptides can also be used  
XX in food stuffs such as infant formula food. The peptides are also  
XX fungicidal and bactericidal and may also be used as preservatives.  
XX Even though native human lactoferrin have been shown to have desired  
XX anti-inflammatory anti-infectious and anti-tumoural properties they  
XX cannot be used clinically on a broad basis because of high production  
XX costs. Therefore, provision of peptides based on lactoferrin would  
XX enable them to be used for the same purposes as lactoferrin at lower  
XX cost.  
XX  
XX Sequence 13 AA;  
SQ  
Query Match 94.4%; Score 67; DB 21; Length 13;  
Best Local Similarity 91.7%; Pred. No. 0.00011;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CFQWQNRNKRVR 12  
Db 2 CFQWQNRNKRVR 13  
RESULT 10  
AAY78036  
ID AAY78036 standard; Peptide; 14 AA.  
XX  
XX AAY78036;  
XX  
XX 25-APR-2000 (first entry)  
DT Human lactoferrin derived peptide SEQ ID NO:36.  
XX  
XX  
XX Human; lactoferrin; modification; infection; inflammation; tumour;  
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;  
KW urinary tract infection; colitis; Candida infection; fungicidal;  
KW bactericidal; preservative.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX WO200001730-A1.  
XX 13-JAN-2000.  
XX 06-JUL-1999; 99WO-S01230.  
XX
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XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX (ASCII-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 12; Page 69; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 14 AA;
Query Match 94.4%; Score 67; DB 21; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKNNMKVR 12
DB 3 CFQWKNNMKVR 14

RESULT 11
AAY78050
ID AAY78050 standard; Peptide; 14 AA.
XX
AC AAY78050;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:50.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 98WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCII-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 15; Page 75; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 14 AA;
Query Match 94.4%; Score 67; DB 21; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKNNMKVR 12
DB 3 CFQWKNNMKVR 14

RESULT 12
AAY78051
ID AAY78051 standard; Peptide; 14 AA.
XX
AC AAY78051;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:51.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 98WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCII-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147388/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX

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PS Claim 18; Page 75; 102pp; English.
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX
SQ Sequence 14 AA;

Query Match          94.4%; Score 67; DB 21; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKRNMRKVR 12
Db 3 CFQWQRNMRKVR 14

RESULT 13
AAR98554
ID AAR98554 standard; Peptide; 15 AA.
XX
AC AAR98554;
XX
DT 12-NOV-1996 (first entry)
XX
DE Peptide for anti-ulcer agent.
XX
KW anti-ulcer agent; low toxicity; stable; heat-resistant.
XX
OS Synthetic.
XX
PN JP08143468-A.
XX
PD 04-JUN-1996.
XX
PF 17-NOV-1994; 94JP-0283869.
XX
PR 17-NOV-1994; 94JP-0283869.
XX
PA (MORG ) MORINAGA MILK IND CO LTD.
XX
DR WPI; 1996-318857/32.
XX
PT Anti-ulcer agent contg. peptide - has low toxicity, is
PT heat-resistant and water-soluble
XX
PS Claim 1; Page 11; 11pp; Japanese.
XX
CC AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
CC administered orally and be produced in large amounts.
XX
SQ Sequence 15 AA;

Query Match          94.4%; Score 67; DB 17; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKRNMRKVR 12
Db 2 CFQWQRNMRKVR 13

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RESULT 14
AAY78035
ID AAY78035 standard; Peptide; 15 AA.
XX
AC AAY78035;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:35.
XX
KW Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001730-A1.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-SE01230.
XX
PR 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
DR WPI; 2000-147398/13.
XX
PT New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 12; Page 69; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX
SQ Sequence 15 AA;

Query Match          94.4%; Score 67; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKRNMRKVR 12
Db 4 CFQWQRNMRKVR 15

RESULT 15
AAY78062
ID AAY78062 standard; Peptide; 15 AA.
XX
AC AAY78062;

```

XX 25-APR-2000 (first entry)
DT Human lactoferrin derived peptide SEQ ID NO:62.
XX
DE Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SB01230.
XX
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 15; Page 81; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX Sequence 15 AA;
SQ

Query Match 94.4%; Score 67; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNNMKVR 12
Db 4 CFQWQNNMKVR 15

Search completed: February 21, 2003, 07:56:44
Job time : 28.093 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds
(without alignments)
39.537 Million cell updates/sec

Title: US-09-743-107b-92

Perfect score: 71

Sequence: 1 CFQWKNNRKVR 12

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*

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5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	94.4	18	1	US-08-204-487-3
2	67	94.4	18	2	US-08-485-948-8
3	67	94.4	18	2	US-08-628-380-8
4	67	94.4	18	2	US-08-475-055-8
5	67	94.4	20	1	US-07-755-161A-3
6	67	94.4	20	1	US-07-891-174-3
7	67	94.4	20	1	US-08-204-487-1
8	67	94.4	20	1	US-08-256-771-24
9	67	94.4	20	1	US-08-256-771-25
10	67	94.4	20	1	US-08-381-984-24
11	67	94.4	20	1	US-08-381-984-25
12	67	94.4	22	4	US-09-508-734-4
13	67	94.4	24	4	US-09-508-734-6
14	67	94.4	25	1	US-07-755-161A-10
15	67	94.4	25	1	US-07-891-174-10
16	67	94.4	25	1	US-08-204-487-7
17	67	94.4	29	4	US-09-508-734-8
18	67	94.4	36	1	US-07-755-161A-8
19	67	94.4	36	1	US-07-891-174-8
20	67	94.4	36	1	US-08-256-771-30
21	67	94.4	36	1	US-08-381-984-29
22	67	94.4	47	2	US-08-464-182A-6
23	67	94.4	47	2	US-08-406-271-6
24	67	94.4	50	2	US-08-693-274A-7
25	67	94.4	52	4	US-09-017-043A-3
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28	67	94.4	54	2	US-08-464-182A-2	Sequence 2, Appli
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31	67	94.4	694	4	US-09-421-632-2	Sequence 2, Appli
32	67	94.4	694	4	US-09-932-190-2	Sequence 2, Appli
33	67	94.4	705	2	US-08-555-640-2	Sequence 2, Appli
34	67	94.4	708	2	US-08-655-640-4	Sequence 4, Appli
35	67	94.4	711	1	US-08-154-019-4	Sequence 4, Appli
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37	67	94.4	711	3	US-08-464-167-4	Sequence 4, Appli
38	67	94.4	711	3	US-09-158-313-4	Sequence 4, Appli
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41	64	90.1	711	1	US-08-250-308-2	Sequence 2, Appli
42	64	90.1	711	1	US-08-453-703-2	Sequence 2, Appli
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45	64	90.1	711	4	US-09-265-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGRAKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIAKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 94.4%; Score 67; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNRKRVR 12
Db 1 CFQWQNRKRVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-485-948-8

Query Match 94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNRKRVR 12
Db 1 CFQWQNRKRVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-628-380-8

Query Match 94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNRKRVR 12
Db 1 CFQWQNRKRVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

```
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Klauber & Jackson
/ STREET: 411 Hackensack Avenue
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,055
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/485,948
/ FILING DATE:
/ APPLICATION NUMBER: 08/488,217
/ FILING DATE: JUNE 7, 1995
/ APPLICATION NUMBER: 08/418,642
/ FILING DATE: APRIL 7, 1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq., David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 947-1-008A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201 343-1684
/ TELEFAX: 201 343-1684
/ TELEX: 133521
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ DESCRIPTION: LP-CL, 8-25
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ US-08-475-055-8
/
/ Query Match 94.4%; Score 67; DB 2; Length 18;
/ Best Local Similarity 91.7%; Pred. No. 9.9e-05;
/ Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 CFQWRNMRKVR 12
/ Db 1 CFQWRNMRKVR 12
/
/ RESULT 5
/ US-07-755-161A-3
/ Sequence 3, Application US/07755161A
/ Patent No. 5304633
/ GENERAL INFORMATION:
/ APPLICANT: Mamoru TOMITA et al.
/ TITLE OF INVENTION: Antimicrobial Peptides and an
/ TITLE OF INVENTION: Antimicrobial Agent
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wenderoth, Lind & Ponack
/ STREET: 805 Fifteenth Street, N.W., #700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
/ COMPUTER: IBM Compatible
/
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: DisplayWrite
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/755,161A
/ FILING DATE: 19910905
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warren M. Cheek Jr.
/ REGISTRATION NUMBER: 33,367
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-8850
/ TELEFAX: 202-371-8856
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: AMINO ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE:
/ HYPOTHETICAL:
/ ANTI-SENSE:
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM:
/ STRAIN:
/ INDIVIDUAL ISOLATE:
/ DEVELOPMENTAL STAGE:
/ HAPLOTYPE:
/ TISSUE TYPE:
/ CELL TYPE:
/ CELL LINE:
/ ORGANELLE:
/ IMMEDIATE SOURCE:
/ LIBRARY:
/ CLONE:
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT:
/ MAP POSITION:
/ UNITS:
/ FEATURE:
/ NAME/KEY: modified site
/ LOCATION: 2
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: /note= "thiol group of
/ OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
/ OTHER INFORMATION: thiol group of Cys residue at location 19"
/ FEATURE:
/ NAME/KEY: modified site
/ LOCATION: 19
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: /note= "thiol group of
/ OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
/ OTHER INFORMATION: thiol group of Cys residue at location 2"
/ PUBLICATION INFORMATION:
/ AUTHORS:
/ TITLE:
/ JOURNAL:
/ VOLUME:
/ ISSUE:
/ PAGES:
/ DATE:
/ DOCUMENT NUMBER:
/ FILING DATE:
/ PUBLICATION DATE:
/ RELEVANT RESIDUES IN SEQ ID NO:
/ US-07-755-161A-3
/
/ Query Match 94.4%; Score 67; DB 1; Length 20;
```

Best Local Similarity 91.7%; Pred. No. 0.00011; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 0;

Qy 1 CFQWRNNRKVR 12
Db 2 CFQWRNNRKVR 13

RESULT 6
US-07-891-174-3
Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
UNITS:
NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWRNNRKVR 12
Db 2 CFQWRNNRKVR 13

RESULT 7
US-08-204-487-1
Sequence 1, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNNRKVR 12
Db 2 CFQWKNNRKVR 13

RESULT 8

US-08-256-771-24
Sequence 24, Application US/08256771
Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256, 771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNNRKVR 12
Db 2 CFQWKNNRKVR 13

RESULT 10

US-08-381-984-24

US-08-256-771-24

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNNRKVR 12
Db 2 CFQWKNNRKVR 13

RESULT 9

US-08-256-771-25
Sequence 25, Application US/08256771
Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256, 771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
OTHER INFORMATION: prevent disulfide bond"

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNNRKVR 12
Db 2 CFQWKNNRKVR 13

Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-24

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNRKR 12
Db 2 CFQWKNRKR 13

RESULT 11
US-08-381-984-25
Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-25

Query Match 94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNRKR 12
Db 2 CFQWKNRKR 13

RESULT 12
US-09-508-734-4
Sequence 4, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast an
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4

```

; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4

Query Match          94.4%; Score 67; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKVR 12
Db 2 CFQWQNRMRKVR 13

RESULT 13
US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6

Query Match          94.4%; Score 67; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKVR 12
Db 3 CFQWQNRMRKVR 14

RESULT 14
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755.161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-755-161A-10

Query Match          94.4%; Score 67; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQNRMRKVR 12
Db 4 CFQWQNRMRKVR 15
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RESULT 15
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21

; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-891-174-10

Query Match 94.4%; Score 67; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00013;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKENMKVR 12
   |||:|||||
Db 4 CFQWQENMKVR 15

Search completed: February 21, 2003, 08:04:26
Job time : 8.93023 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 08:08:15 ; Search time 6.88372 Seconds
(without alignments)
54.162 Million cell updates/sec

Title: US-09-743-107B-92

Perfect score: 71

Sequence: 1 CFQWRNMRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 155504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	94.4	15	9	US-09-798-869-2
2	67	94.4	25	9	US-09-798-869-20
3	67	94.4	694	9	US-10-023-096-2
4	59	83.1	15	9	US-09-798-869-6
5	50	70.4	15	9	US-09-798-869-3
6	50	70.4	25	9	US-09-798-869-23
7	42	59.2	15	9	US-09-798-869-7
8	41	57.7	15	9	US-09-798-869-4
9	41	57.7	25	9	US-09-798-869-22
10	39	54.9	333	9	US-09-796-753-26
11	38	53.5	15	9	US-09-798-869-8
12	38	53.5	15	9	US-09-798-869-29
13	38	53.5	15	9	US-09-798-869-30
14	38	53.5	21	10	US-09-864-761-47985
15	38	53.5	489	9	US-09-888-320-2
16	37	52.1	77	10	US-09-864-761-41002
17	37	52.1	86	9	US-09-738-626-5715
18	37	52.1	184	10	US-09-925-301-1248
19	37	52.1	338	9	US-09-978-295A-119

20	37	52.1	338	9	US-09-978-697-119	Sequence 119, App
21	37	52.1	338	9	US-09-978-192A-119	Sequence 119, App
22	37	52.1	338	9	US-09-999-832A-119	Sequence 119, App
23	37	52.1	338	9	US-09-978-189-119	Sequence 119, App
24	37	52.1	553	9	US-09-796-753-14	Sequence 14, Appl
25	37	52.1	553	10	US-09-981-649A-6	Sequence 6, Appli
26	37	52.1	553	10	US-09-981-649A-24	Sequence 24, Appl
27	37	52.1	554	10	US-09-981-649A-30	Sequence 30, Appl
28	37	52.1	554	10	US-09-981-649A-32	Sequence 32, Appl
29	37	52.1	559	10	US-09-981-649A-28	Sequence 28, Appl
30	35	49.3	301	9	US-10-080-960-11	Sequence 11, Appl
31	35	49.3	302	10	US-09-948-078-2	Sequence 2, Appli
32	35	49.3	351	10	US-09-853-625B-16	Sequence 16, Appl
33	35	49.3	1013	9	US-10-028-072-38	Sequence 38, Appl
34	35	49.3	1013	9	US-10-121-049-38	Sequence 38, Appl
35	35	49.3	1013	9	US-10-123-904-38	Sequence 38, Appl
36	35	49.3	1013	9	US-10-140-470-38	Sequence 38, Appl
37	35	49.3	1013	9	US-10-175-746-38	Sequence 38, Appl
38	35	49.3	1013	9	US-10-176-918-38	Sequence 38, Appl
39	35	49.3	1013	9	US-10-176-921-38	Sequence 38, Appl
40	35	49.3	1013	9	US-10-137-865-38	Sequence 38, Appl
41	35	49.3	1013	9	US-10-140-474-38	Sequence 38, Appl
42	34	47.9	62	10	US-09-815-242-12129	Sequence 12129, A
43	34	47.9	62	10	US-09-815-242-13026	Sequence 13026, A
44	34	47.9	509	10	US-09-879-957-194	Sequence 194, App
45	34	47.9	846	9	US-10-051-409-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PPT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 94.4%; Score 67; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 5.1e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWRNMRKVR 12
|||:|||||
DB 3 CFQWRNMRKVR 14

RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON

Query Match 70.4%; Score 50; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.028;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKNNRKV 11
|:|:|:|:
Db 3 CYQWQNRKVL 13

RESULT 6

US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 70.4%; Score 50; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.045;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKNNRKV 11
|:|:|:|:
Db 3 CYQWQNRKVL 13

RESULT 7

US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 59.2%; Score 42; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.55;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKNNRKV 11
|:|:|:|:
Db 3 CYQWQNRKVL 13

RESULT 8

US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 57.7%; Score 41; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.8;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNNRKV 11
|:|:|:|:
Db 3 CLRWQNRKVL 13

RESULT 9

US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 57.7%; Score 41; DB 9; Length 25;
Best Local Similarity 54.5%; Pred. No. 1.3;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNNRKV 11
|:|:|:|:
Db 3 CLRWQNRKVL 13

RESULT 10
US-09-796-753-26
; Sequence 26, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
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; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
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; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 26
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Mouse
US-09-796-753-26

Query Match 54.9%; Score 39; DB 9; Length 333;
Best Local Similarity 54.5%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy 1 CFQWKRNKRV 11
| : | | | : |
Db 48 CYQWKRNKGV 58
| : | | | : |
RESULT 11
US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8

Query Match 53.5%; Score 38; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 2.4;
Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy 1 CFQWKRNKRV 11
| : | | | : |
Db 3 CLRQWEMKRV 13
| : | | | : |

RESULT 12
US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 53.5%; Score 38; DB 9; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.4;
Matches 5; Conservative 4; Mismatches 2; Indels 2; Gaps 0;

Qy 1 CFQWKRNKRV 11
| : | | | : |

Db 3 CFWQWRMKKL 13

RESULT 13

US-09-798-869-30
; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVINEBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30

Query Match 53.5%; Score 38; DB 9; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.4;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFWQWRMKKV 11

|||:|:

Db 3 CFWQWRMKKL 13

RESULT 14

US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47985
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL096701.14
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUATE 1.00e-06
US-09-864-761-47985

Query Match 53.5%; Score 38; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFWQWR 6

|||:|:

Db 16 CFWQWR 21

RESULT 15

US-09-888-320-2
; Sequence 2, Application US/09888320
; Publication No. US20030013090A1
; GENERAL INFORMATION:
; APPLICANT: Barry III, Clifton E.
; APPLICANT: DeBarber, Andrea E.
; APPLICANT: Mdulili, Khisimuzi
; APPLICANT: Bekker, Linda-Gail
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
; FILE REFERENCE: 015280-413100US
; CURRENT APPLICATION NUMBER: US/09/888,320
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/214,187
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type Etad monooxygenase (RV3854C, EthA)
US-09-888-320-2

Query Match 53.5%; Score 38; DB 9; Length 489;
Best Local Similarity 54.5%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFWQWRMKKV 11

|||:|:

Db 253 COKWPRVRKMK 263

Search completed: February 21, 2003, 08:11:56
Job time : 6.88372 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:48:01 ; Search time 10.6047 Seconds
(without alignments)
108.784 Million cell updates/sec

Title: US-09-743-107B-92

Perfect score: 71

Sequence: 1 CFQWKNRKR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:.*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	94.4	711	1 TFHUL	lactotransferrin precursor
2	50	70.4	708	2 JC2323	lactoferrin - goat
3	47	66.2	33	2 S52107	lactoferrin - sheep
4	45	63.4	275	2 T22597	hypothetical prote
5	41	57.7	206	2 H97451	pyridoxamine 5'-ph
6	41	57.7	206	2 AB2670	probable pyridoxam
7	41	57.7	208	2 AG3441	hypothetical prote
8	41	57.7	511	2 AB0858	hypothetical prote
9	41	57.7	707	1 A28438	lactoferrin precu
10	40	56.3	584	2 C94325	hypothetical prote
11	40	56.3	4568	2 T08030	dyein beta heavy
12	39	54.9	447	2 T18633	hypothetical prote
13	39	54.9	759	2 G86506	hypothetical prote
14	39	54.9	759	2 G72115	hypothetical prote
15	38	53.5	60	2 A48336	ribosomal protein
16	38	53.5	62	2 AH1301	ribosomal protein
17	38	53.5	62	2 AH1673	ribosomal protein
18	38	53.5	267	2 S77802	hypothetical prote
19	38	53.5	298	2 A23466	hypothetical prote
20	38	53.5	393	2 B64639	3-deoxy-manno-octu
21	38	53.5	489	2 C70655	probable monooxyge
22	38	53.5	583	2 T01470	diphosphate-fructo
23	37	52.1	205	2 E90094	26S proteasome SU
24	37	52.1	214	2 S07989	vif protein - simi
25	37	52.1	274	2 B50950	apolipoprotein B-1
26	37	52.1	357	2 T22879	hypothetical prote
27	37	52.1	513	2 E86156	T14P4.7 protein -
28	37	52.1	518	2 B84514	probable cytochrom
29	37	52.1	536	2 T24218	hypothetical prote

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S

R/Cho, Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AA60324.1; PID:G467237

R/Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148; T, 150-422, C, 424-711 <REY>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactofe

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:G263311; PIDN:AA624877.1; PID:G263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <STI>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, X, 30-31 <ST2>

R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Accession: S07160
A;Molecule type: mRNA
A;Residues: 436-487, 'A', 489-711 <RAD>
A;Cross-references: EMBL:W18642; NID:9186815; PIDN:AAA86665.1; PID:9386855
R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
A;Reference number: A61169; MUID:91235214; PMID:1674448
A;Accession: A61169
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 3-701, 'SWKPNV' <PAN>
A;Experimental source: normal breast tissue
R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, P.; Legrand, D.; Spik, G.;
Eur. J. Biochem. 145, 659-666, 1984
A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
A;Reference number: A31000; MUID:85076667; PMID:6510420
A;Accession: A31000
A;Molecule type: protein
A;Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
A;Note: this is the final paper in a series
R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Eur. J. Biochem. 241, 303-308, 1996
A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity
A;Reference number: S74119; MUID:97054624; PMID:8898921
A;Accession: S74119
A;Molecule type: protein
A;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
A;Experimental source: neutrophil granulocytes
C;Genetics:
A;Gene: GDB:LNFB
A;Cross-references: GDB:119368; OMIM:150210
A;Map position: 3q21-3q23
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-711/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;729-6539-56135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e
F;157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;1365-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #statu

Query Match 94.4%; Score 67; DB 1; Length 711;
Best Local Similarity 91.7%; Pred. No. 0.00075;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNRKVK 12
Db 39 CFQWQNRKVR 50
|||:|||||
|||:|||||

RESULT 2
JC2323
lactoferrin - goat
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: JC2323
R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
A;Reference number: JC2323; MUID:94380047; PMID:8093048
A;Accession: JC2323
A;Molecule type: mRNA
A;Residues: 1-708 <LEP>
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
F;553-686/Domain: transferrin repeat homology <TRH2>
F;1252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.4%; Score 50; DB 2; Length 708;
Best Local Similarity 63.6%; Pred. No. 0.072;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWKNRKVK 11
Db 38 CFQWQNRKVK 48
|||:|||||
|||:|||||

RESULT 3
S52107
lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samouri, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet
A;Reference number: S52107; MUID:95127729; PMID:7827104
A;Accession: S52107
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-33 <QIA>
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication

Query Match 66.2%; Score 47; DB 2; Length 33;
Best Local Similarity 54.5%; Pred. No. 0.12;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWKNRKVK 11
Db 19 CFQWQNRKVK 29
|||:|||||
|||:|||||

RESULT 4
T22597
hypothetical protein F53H4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
R;Dobson, R.
Submitted to the EMBL Data Library, October 1996
A;Reference number: Z19587
A;Accession: T22597
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-275 <WIL>
A;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
A;Experimental source: clone F53H4
C;Genetics:
A;Gene: CESP:F53H4.4
A;Map position: X
A;Introns: 67/1; 153/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4

Query Match 63.4%; Score 45; DB 2; Length 275;
Best Local Similarity 72.7%; Pred. No. 2.2;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FQWKNRKVR 12
Db 262 FQWKNRKVR 272
|||:|||||
|||:|||||

RESULT 5
H97451
Pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (s
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: H97451
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldma

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* strain C58, 2001
 A:Reference number: A97359; PMID:11743194
 A:Accession: H97451
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-206 <KUR>
 A:Cross-references: GB:AB007869; PIDN:AAK8569.1; PID:gl5155733; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR C1381
 A:Map position: circular chromosome
 C:Superfamily: pyridoxamine-phosphate oxidase

Query Match 57.7%; Score 41; DB 2; Length 206;
 Best Local Similarity 58.3%; Pred. No. 8.2;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKRNMKVR 12
 |||||
 Db 88 CFHWKSLRRQVR 99
 |||||

RESULT 6
 AB2670
 A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AB2670
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-206 <KUR>
 A:Cross-references: GB:AB008688; PIDN:AAU41776.1; PID:gl7739129; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: pdxH
 A:Map position: circular chromosome
 C:Superfamily: pyridoxamine-phosphate oxidase

Query Match 57.7%; Score 41; DB 2; Length 206;
 Best Local Similarity 58.3%; Pred. No. 8.2;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKRNMKVR 12
 |||||
 Db 88 CFHWKSLRRQVR 99
 |||||

RESULT 7
 AG3441
 A:Title: probable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - *Brucella melitensis* (strain 16M)
 C:Species: *Brucella melitensis*
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
 A:Accession: AG3441
 A:Reference number: A97359; PMID:11743194
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-206 <KUR>
 A:Cross-references: GB:AB008917; PIDN:AAU52698.1; PID:gl7983525; GSPDB:GN00190

A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BME11517
 A:Map position: I
 C:Superfamily: pyridoxamine-phosphate oxidase
 C:Keywords: oxidoreductase

Query Match 57.7%; Score 41; DB 2; Length 208;
 Best Local Similarity 58.3%; Pred. No. 8.3;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKRNMKVR 12
 |||||
 Db 90 CFHWKSLRRQVR 101
 |||||

RESULT 8
 AB0958
 A:Title: hypothetical protein STY3070 [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhimurium
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhimurium
 A:Note: this species has also been called *Salmonella typhimurium*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AB0958
 A:Reference number: AB0958
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-511 <PAR>
 A:Cross-references: GB:AL513392; PIDN:CAD06049.1; PID:gl6504016; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY3070

Query Match 57.7%; Score 41; DB 2; Length 511;
 Best Local Similarity 58.3%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWKRNMKVR 12
 |||||
 Db 350 CFADWMMKAKVR 361
 |||||

RESULT 9
 A28438
 A:Title: lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C:Species: *Mus musculus* (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A28438; A41205
 A:Reference number: A28438; A41205
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-707 <PEN>
 A:Cross-references: EMBL:J03298
 A:Map position: 3-707 <PEN>
 A:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:1-19/Domain: signal sequence #atdata predicted <SIG>

F:20-707/Product: lactotransferrin #status predicted <MAT>
 F:358-695/Domain: transferrin repeat homology <TRH2>
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.7%; Score 41; DB 1; Length 707;
 Best Local Similarity 54.5%; Pred. No. 28;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOWKRNMRKV 11
 |||:|:|:
 DB 37 CLFQWQEMRKV 47

RESULT 10

C84325
 hypothetical protein Vngl732c [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: C84325
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laeky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: C84325
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-584 <STO>
 A:Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: VNG1732C

Query Match 56.3%; Score 40; DB 2; Length 584;
 Best Local Similarity 41.7%; Pred. No. 34;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOWKRNMRKV 12
 |||:|:|:
 DB 445 CFTWKDMERK 456

RESULT 11

T08030
 dynein beta heavy chain - Chlamydomonas reinhardtii
 C:Species: Chlamydomonas reinhardtii
 C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
 C:Accession: T08030
 R:Mitchell, D.R.; Brown, K.S.
 J. Cell Sci. 107, 635-644, 1994
 A:Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
 A:Reference number: Z16302; MUID:94274778; PMID:8006077
 A:Accession: T08030
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-4568 <MIT>
 A:Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:9514215
 A:Experimental source: strain 21gr
 C:Genetics:
 A:Gene: ODA4
 A:Map position: IX
 A:Introns: 49/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
 3334/3; 3686/3; 3892/3; 4240/3
 C:Superfamily: dynein heavy chain, ciliary
 C:Keywords: nucleotide binding; P-loop
 F:1919-1926/Region: nucleotide-binding motif A (P-loop)
 F:2202-2209/Region: nucleotide-binding motif A (P-loop)
 F:2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 56.3%; Score 40; DB 2; Length 4568;
 Best Local Similarity 41.7%; Pred. No. 2.5e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOWKRNMRKV 12
 |||:|:|:
 DB 1852 CFQWQSLRYIQ 1863

RESULT 12

T18633
 hypothetical protein M18.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T18633; T23799
 R:Sims, M.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: Z18999
 A:Accession: T18633
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-447 <WIL>
 A:Cross-references: EMBL:Z69634; PIDN:CAA93457.1; GSPDB:GN000022; CESP:M18.8
 A:Experimental source: clone B0001
 R:Steward, C.
 submitted to the EMBL Data Library, January 1996

A:Reference number: Z19800
 A:Accession: T23799
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-447 <W12>
 A:Cross-references: EMBL:Z68507; PIDN:CAA92831.1; GSPDB:GN000022; CESP:M18.8
 A:Experimental source: clone M18
 C:Genetics:
 A:Gene: CESP:M18.8
 A:Map position: 4
 A:Introns: 41/3; 137/1; 326/3; 434/2

Query Match 54.9%; Score 39; DB 2; Length 447;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 WKRNMRKV 11
 |||:|:|:
 DB 291 WKRNLRV 298

RESULT 13

G86506
 hypothetical protein CFJ0126 [imported] - Chlamydomophila pneumoniae (strain J138)
 C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C:Accession: G86506
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: G86506
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-759 <STO>
 A:Cross-references: GB:BA000008; NID:g8978500; PIDN:BAA98337.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: CFJ0126

Query Match 54.9%; Score 39; DB 2; Length 759;
 Best Local Similarity 66.7%; Pred. No. 66;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWKNMRKV 11
 |||:|:|:
 DB 488 QWKNLRDV 496

RESULT 14

G72115
hypothetical protein CP0646 [imported] - Chlamydomydia pneumoniae (strains CWL029 and AR
C:Species: Chlamydomydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: G72115; F81554
R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Pan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: G72115
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-759 <ARN>
A:Cross-references: GB:AE001599; GB:AE001363; MID:g4376387; PIDN:AAF18279.1; PID:g437639
A:Experimental source: strain CWL029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: F81554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-759 <REA>
A:Cross-references: GB:AE002222; GB:AE002161; MID:g7189553; PIDN:AAF38461.1; PID:g718956
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0126; CP0646

Query Match 54.9%; Score 39; DB 2; Length 759;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWKNMKV 11
|||:|:|
DB 488 QWKNLRDV 496

RESULT 15
A48396
ribosomal protein L28 - Bacillus stearothermophilus
C:Species: Bacillus stearothermophilus
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 21-Aug-1998
C:Accession: A48396
R:Kruft, V.; Kapp, U.; Wittmann-Liebold, B.
Biochimie 73, 855-860, 1991
A:Title: Characterization and primary structure of proteins L28, L33 and L34 from Bacill
A:Reference number: A48396; MUID:92075758; PMID:1742360
A:Accession: A48396
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-60 <KRU>
A:Note: sequence extracted from NCBI backbone (NCBIP:69662)
C:Superfamily: Escherichia coli ribosomal protein L28

Query Match 53.5%; Score 38; DB 2; Length 60;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WKNMKV 12
|||:|:|
DB 27 WKANLQVR 35

Search completed: February 21, 2003, 08:02:46
Job time : 10.6047 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:28:06 ; Search time 5.2093 Seconds
(without alignments)
95.544 Million cell updates/sec

Title: US-09-743-107b-92
Perfect score: 71
Sequence: 1 CFWQKNNRKYR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	94.4	711	TRFL_HUMAN	P02788 homo sapien
2	50	70.4	708	TRFL_CAMDR	Q9tum0 camelus dro
3	50	70.4	708	TRFL_CAPHI	Q29477 capra hircu
4	42	59.2	695	1 TRFL_HORSE	O77811 equus cabal
5	41	57.7	62	1 RL28_THETN	O8r9u1 thermoanaer
6	41	57.7	707	1 TRFL_MOUSE	P08071 mus musculu
7	40	56.3	4568	1 DYHB_CHLRE	Q39565 chlamydomon
8	39	54.9	292	1 NLA_DROME	Q9xz18 drosophila
9	38	53.5	60	1 RL28_BACST	P23374 bacillus st
10	38	53.5	62	1 RL28_LISMO	Q92aj2 listeria mo
11	38	53.5	146	1 RPOB_LIBAF	P41187 liberibacte
12	38	53.5	267	1 Y125_MYCCA	P53661 mycoplasma
13	37	52.1	214	1 VIF_SIVS4	P12505 simian immu
14	37	52.1	783	1 YNR2_CAEEL	Q21588 caenorhabdi
15	36	50.7	365	1 1A3*_HUMAN	P30453 homo sapien
16	36	50.7	455	1 YKYL_CAEEL	Q19910 caenorhabdi
17	36	50.7	485	1 GLGA_BACST	O08328 bacillus st
18	36	50.7	502	1 C932_SOYBN	Q42799 glycine max
19	36	50.7	509	1 C931_SOYBN	Q42798 glycine max
20	36	50.7	510	1 C933_SOYBN	O81973 glycine max
21	36	50.7	528	1 CAX2_ARATH	O38798 arabidopsis
22	36	50.7	530	1 CAX1_ARATH	P29402 arabidopsis
23	36	50.7	728	1 KDGI_ARATH	Q39017 arabidopsis
24	36	50.7	749	1 VP4_ROTGA	Q04916 rotavirus (
25	36	50.7	1135	1 PHYC_SORBI	Q93528 sorghum bic
26	35	49.3	151	1 SYB2_RHIME	O923c1 rhizobium m
27	35	49.3	215	1 VIF_HV2SB	P12452 human immu
28	35	49.3	215	1 VIF_HV2ST	P20878 human immu
29	35	49.3	343	1 SP2D_BACSU	P07372 bacillus su
30	35	49.3	344	1 SP2D_BACAM	P13251 bacillus am
31	35	49.3	351	1 NOV_CHICK	P28686 gallus gall
32	35	49.3	358	1 DDL_ENTHR	Q47827 enterococu
33	35	49.3	398	1 YK13_CAEEL	P34337 caenorhabdi

ALIGNMENTS

RESULT 1

ID	TRFL_HUMAN	STANDARD	PRT	711 AA
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H123; Q96K24;			
AC	Q96K25;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C].			
GN	LfR OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RC	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cho Y.Y.;			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Connely O.M.;			
RT	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RT	sequences.";			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA cloning and sequence analysis of human lactoferrin.";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

Q9vfn2 drosophila
Q9pj19 chlamydia m
Q9ute7 schizosacch
P35649 eikenella c
P58306 thermoplasma
Q9ulc6 homo sapien
Q99up4 staphylococ
P29328 ovine aries
Q10353 schizosacch
P43488 mus musculu
P19506 simian immu
Q55185 synechocyst

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE-Mammary Gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=8507667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
R LeGrand D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
R Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
alignment of the cyanogen bromide fragments and characterization of
N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
R Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
lactotransferrin.";
RL FEBS Lett. 142:107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
R Nhan M., Parnell L., Dedhia A., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
R Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
R Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sacripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
R Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
binding properties and crystal structure of the histidine-
253--methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;

RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
R Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
R El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejtmancik J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
RN [21]
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
CC
RP FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC
RP SUBUNIT: MONOMER
CC
RP SUBCELLULAR LOCATION: Secreted
CC
RP DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC
RP SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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EMBL; X53961; CAA37914.1; -
EMBL; U07643; AAB60324.1; -
EMBL; M93150; AAA36159.1; -
EMBL; M83202; AAA59511.1; -
EMBL; M83205; AAA58656.1; -
EMBL; M18642; AAA86665.1; -
EMBL; AF332168; AAG48753.1; -
EMBL; BC015822; AAH15822.1; -
EMBL; BC015823; AAH15823.1; -
EMBL; M73700; AAA59479.1; -
EMBL; X52941; CAA37116.1; -
EMBL; U95626; AAB57795.1; -
PIR; S11228; TFHUL.
DR PDB; 1LCF; 31-AUG-94.
DR PDB; 1LCT; 31-OCT-93.
DR PDB; 1LFG; 31-JUL-94.
DR PDB; 1LFH; 31-OCT-93.
DR PDB; 1LFH; 31-OCT-93.
DR PDB; 1LGB; 31-AUG-94.
DR PDB; 1LGC; 31-AUG-94.
DR PDB; 1BKA; 08-NOV-96.
DR PDB; 1DSN; 08-MAR-96.
DR PDB; 1HSE; 12-MAR-97.
DR PDB; 1VFD; 21-APR-97.


```
Query Match          94.4%; Score 67; DB 1; Length 711;
Best Local Similarity 91.7%; Pred. No. 0.0002;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWKRNRKVR 12
   |||||:|||||
DB 39 CFQWRNRKVR 50

RESULT 2
TRFL CAMDR
ID TRFL CAMDR STANDARD; PRT; 708 AA.
AC QPTUMQ; QNZS5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Camelus dromedarius (Dromedary) (Arabic camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=Sonali; TISSUE=Lactating mammary gland;
RA Kapteer S.R.; Ackermann M.; Farah Z.; Puhani Z.;
RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
RL Int. Dairy J. 9:481-486(1999).
RN 2
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Paramasivam M.; Srinivasan A.; Singh R.; Sahani M.S.; Singh T.P.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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CC
DR EMBL; AJ131674; CAB53387.1; -.
DR EMBL; AF165879; AAF82241.1; -.
DR HSSP; O77811; 1B1X.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN 1; 2.
DR PROSITE; PS00206; TRANSFERRIN 2; 2.
DR PROSITE; PS00207; TRANSFERRIN 3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 708 LACTOTRANSFERRIN.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT DISULFID 28 64 BY SIMILARITY.
FT DISULFID 38 55 BY SIMILARITY.
FT DISULFID 134 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.

Query Match          70.4%; Score 50; DB 1; Length 708;
Best Local Similarity 66.7%; Pred. No. 0.22;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWRNRKVR 12
   |||||:|||||
DB 38 CAQWRNRKVR 49

RESULT 3
TRFL CAPHI
ID TRFL CAPHI STANDARD; PRT; 708 AA.
AC Q29477; Q29479;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (lactoferrin).
GN LTF.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Lee T.; Yu S.; Kim S.; Lee K.; Yu D.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN 2
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=94380047; PubMed=8093048;
RT le Provost F.; Nocart M.; Guerin G.; Martin P.;
RT "Characterization of the goat lactoferrin cDNA. Assignment of the
RT relevant locus to bovine U12 syntenic group.";
RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
```

CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: U53857; AAA97958.1; --
 CC EMBL: X78902; CAA55517.1; --
 CC HSP: 077698; 1CE2.
 CC InterPro: IPR001156; Transferrin.
 CC Pfam: PF00405; transferrin; 2.
 CC PRINTS: PR00422; TRANSFERRIN.
 CC SMART: SM00094; TR FER; 2.
 CC PROSITE: PS00205; TRANSFERRIN_1; 2.
 CC PROSITE: PS00206; TRANSFERRIN_2; 2.
 CC PROSITE: PS00207; TRANSFERRIN_3; 2.
 CC Transports; Iron transport; Metal-binding; Repeat;
 CC Signal.
 CC -----
 CC SIGNAL 1 19 BY SIMILARITY.
 CC CHAIN 20 708 LACTOTRANSFERRIN.
 CC REPEAT 20 363 1.
 CC REPEAT 364 708 2.
 CC DISULFID 28 64 BY SIMILARITY.
 CC DISULFID 38 55 BY SIMILARITY.
 CC DISULFID 134 217 BY SIMILARITY.
 CC DISULFID 176 192 BY SIMILARITY.
 CC DISULFID 189 200 BY SIMILARITY.
 CC DISULFID 250 264 BY SIMILARITY.
 CC DISULFID 367 399 BY SIMILARITY.
 CC DISULFID 377 390 BY SIMILARITY.
 CC DISULFID 424 703 BY SIMILARITY.
 CC DISULFID 444 666 BY SIMILARITY.
 CC DISULFID 476 551 BY SIMILARITY.
 CC DISULFID 500 594 BY SIMILARITY.
 CC DISULFID 510 524 BY SIMILARITY.
 CC DISULFID 521 534 BY SIMILARITY.
 CC DISULFID 592 606 BY SIMILARITY.
 CC DISULFID 644 649 BY SIMILARITY.
 CC METAL 79 IRON 1 (BY SIMILARITY).
 CC METAL 111 IRON 1 (BY SIMILARITY).
 CC METAL 211 IRON 1 (BY SIMILARITY).
 CC METAL 272 IRON 1 (BY SIMILARITY).
 CC METAL 414 IRON 2 (BY SIMILARITY).
 CC METAL 452 IRON 2 (BY SIMILARITY).
 CC METAL 545 IRON 2 (BY SIMILARITY).
 CC METAL 614 IRON 2 (BY SIMILARITY).
 CC BINDING 140 ANION (BY SIMILARITY).
 CC BINDING 482 ANION (BY SIMILARITY).
 CC CARBOHYD 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CONFLICT 56 I -> V (IN REF. 2).
 CC CONFLICT 88 L -> R (IN REF. 2).
 CC CONFLICT 124 F -> K (IN REF. 2).
 CC CONFLICT 154 F -> P (IN REF. 2).
 CC CONFLICT 304 S -> R (IN REF. 2).
 CC CONFLICT 414 D -> G (IN REF. 2).
 CC SEQUENCE 708 AA; 77358 MW; P2EDA3C6339960D CRC64;
 CC -----
 CC Query Match 70.4%; Score 50; DB 1; Length 708;
 CC Best Local Similarity 63.6%; Pred. No. 0.22;
 CC Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC 1 CFQWKNRKRKV 11
 CC 38 CYQWQRNRKRL 48

RESULT 4
 TRFL HORSE
 ID TRFL HORSE STANDARD; PRT; 695 AA.
 AC 077811;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).
 GN LTF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN (1)_TaxID=9796;
 RN SEQUENCE FROM N.A.
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "cDNA sequence of mare lactoferrin";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Milk;
 RX MEDLINE=99296631; PubMed=10366507;
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
 resolution.";
 RL J. Mol. Biol. 289:303-317(1999).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: AJ010930; CAA09407.1; --
 CC FDB: 1BIX; 02-DEC-98.
 CC FDB: 1B7U; 02-FEB-99.
 CC FDB: 1B7Z; 02-FEB-99.
 CC InterPro: IPR001156; Transferrin.
 CC Pfam: PF00405; transferrin; 2.
 CC PRINTS: PR00422; TRANSFERRIN.
 CC SMART: SM00094; TR FER; 2.
 CC PROSITE: PS00205; TRANSFERRIN_1; 2.
 CC PROSITE: PS00206; TRANSFERRIN_2; 2.
 CC PROSITE: PS00207; TRANSFERRIN_3; 1.
 CC Transports; Iron transport; Metal-binding; Repeat;
 CC Signal; 3D-structure.
 CC NON_TER 1 1
 CC SIGNAL <1 6
 CC CHAIN 7 695 LACTOTRANSFERRIN.
 CC REPEAT 7 350 1.
 CC REPEAT 351 695 2.
 CC DISULFID 15 51
 CC DISULFID 25 42
 CC DISULFID 121 204
 CC DISULFID 163 179
 CC DISULFID 166 189
 CC DISULFID 176 187
 CC DISULFID 237 251
 CC DISULFID 354 386
 CC DISULFID 364 377
 CC DISULFID 411 690
 CC DISULFID 431 653


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FT REPEAT 358 707
FT DISULFID 27 63
FT DISULFID 37 54
FT DISULFID 133 216
FT DISULFID 175 191
FT DISULFID 188 199
FT DISULFID 249 263
FT DISULFID 366 398
FT DISULFID 376 389
FT DISULFID 423 702
FT DISULFID 443 665
FT DISULFID 475 550
FT DISULFID 499 693
FT DISULFID 509 523
FT DISULFID 520 533
FT DISULFID 591 605
FT DISULFID 643 648
FT METAL 78 78
FT METAL 110 110
FT METAL 210 210
FT METAL 271 271
FT METAL 413 413
FT METAL 451 451
FT METAL 544 544
FT METAL 613 613
FT METAL 139 139
FT BINDING 481 481
FT BINDING 118 118
FT CARBOHYD 494 494
FT CONFLICT 1 2
FT CONFLICT 25 25
FT CONFLICT 82 82
FT CONFLICT 359 359
FT CONFLICT 382 382
FT CONFLICT 449 449
FT CONFLICT 629 629
FT CONFLICT 707 707
FT SEQUENCE 707 AA; 77865 MW; F26AE0340AC19A8 CRC64;

Query Match 57.7%; Score 41; DB 1; Length 707;
Best Local Similarity 54.5%; Pred. No. 8.7;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CFQWKNRKRV 11
DB 37 CLRQWENRKV 47

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RESULT 7
ID_DYHB CHLRE STANDARD; PRT; 4568 AA.
AC Q3955;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein beta chain, flagellar outer arm.
GN ODA4 OR ODA-4 OR SUP1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21GR;
RX MEDLINE=94274778; PubMed=8006077;
RA Michell D.R., Brown K.S.,
RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
chain genes."
RL J. Cell Sci. 107:635-644 (1994).
CC -1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC DYNEIN HAS ATPASE ACTIVITY.
CC -1- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.

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CC -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U02963; AAA19956.1;
CC InterPro; IPR004273; Dynein_heavy;
CC Pfam; PF03028; Dynein_heavy; 1.
CC Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
CC Coiled coil.
CC FT DOMAIN 277 293 COILED COIL (POTENTIAL).
CC FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
CC FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
CC FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
CC FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
CC FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
CC FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
CC FT DOMAIN 3105 3162 COILED COIL (POTENTIAL).
CC FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
CC FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
CC FT NP_BIND 1919 1926 ATP (POTENTIAL).
CC FT NP_BIND 2202 2209 ATP (POTENTIAL).
CC FT NP_BIND 2530 2537 ATP (POTENTIAL).
CC FT NP_BIND 2879 2886 ATP (POTENTIAL).
CC FT SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 56.3%; Score 40; DB 1; Length 4568;
Best Local Similarity 41.7%; Pred. No. 92;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 CFQWKNRKRV 12
DB 1852 CFQWQSLRYIQ 1863

RESULT 8
ID_NLA DROME STANDARD; PRT; 292 AA.
AC Q9XZL8; Q9V391;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nebula protein.
GN NLA OR CG6072.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA McCormick A.V., Goldberg M.L.;
RT "Gene required for elongation of meiosis I spindle in Drosophila
females."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M.E., Kalush C., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.F., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*."
 RT Science 287:2185-2195(2000).
 RL
 CC -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
 CC
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 CC
 CC EMBL; AF147700; AAD33987.1; -;
 DR EMBL; AE003712; AAF5285.1; -;
 DR Flybase; FBgn0026629; nla.
 SQ SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
 Query Match 54.9%; Score 39; DB 1; Length 292;
 Best Local Similarity 54.5%; Pred. No. 7.9;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FOWLRNMRKVR 12
 DB 150 FOWLRNMRKVR 160
 RESULT 9
 ID RL28_BACST STANDARD; PRT; 60 AA.
 AC P23374;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L28.
 GN RPB.
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillales; Geobacillus.
 CC NCBI TaxID=1422;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92075758; PubMed=1742360;
 RA Krufft V., Kapp U., Wittmann-Liebold B.;
 RT "Characterization and primary structure of proteins L28, L33 and L34
 RT from *Bacillus stearothermophilus* ribosomes.";
 RL Biochimie 73:855-860(1991).

CC -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
 DR PIR; A48396; A48396.
 DR InterPro; IPR001383; Ribosomal L28.
 DR Pfam; PF00830; Ribosomal L28; 1.
 DR TIGRFAMs; TIGR00009; L28; 1.
 KW Ribosomal protein.
 FT INIT MET 0
 SQ SEQUENCE 60 AA; 6810 MW; 2AD9161CD60B82F4 CRC64;
 Query Match 53.5%; Score 38; DB 1; Length 60;
 Best Local Similarity 66.7%; Pred. No. 2.3;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 WGRNMRKVR 12
 DB 27 WGRNMRKVR 35
 RESULT 10
 ID RL28_LISMO STANDARD; PRT; 62 AA.
 AC Q92AJ2;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L28.
 GN RPB OR LMO1816 OR LMO1930.
 OS Listeria monocytogenes, and
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 CC NCBI TaxID=1639, 1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=L.monocytogenes, and L.innocua;
 RC STRAIN=EG-e / Serovar 1/2a, and CLIP 11262 / Serovar 6a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Francou P., Blocher H., Brandt P., Chakraborty T.,
 RA Baquer P., Berche P., Blocher H., Brandt P., Chakraborty T.,
 RA Charbit A., Cherouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Donann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst J., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schluster T., Simoes N., Tisrez A.,
 RA Vaquer-Solana J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria* species.";
 RL Science 294:849-852(2001).
 CC -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
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 CC
 CC EMBL; AL591981; CAC99894.1; -;
 DR EMBL; AL596170; CAC97160.1; -;
 DR Listlist; LMO1930; -;
 DR Listlist; LMO01816; -;
 DR InterPro; IPR001383; Ribosomal L28.
 DR Pfam; PF00830; Ribosomal L28; 1.
 DR TIGRFAMs; TIGR00009; L28; 1.
 KW Ribosomal protein; Complete proteome.
 RP SEQUENCE 62 AA; 6931 MW; AA43DE039213C562 CRC64;
 Query Match 53.5%; Score 38; DB 1; Length 62;
 Best Local Similarity 66.7%; Pred. No. 2.3;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 4 WKRNKVR 12
DB 29 WKANLQVR 37

RESULT 11
RPOB LIBAF STANDARD; PRT; 146 AA.
AC P4187;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta chain (BC 2.7.7.6) (Transcriptase
  beta chain) (RNA polymerase beta subunit) (Fragment).
GN RPOB.
OS Liberibacter africanus (Liberibacter africanum).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Candidatus Liberibacter.
OX NCBI_TaxID=34020;
RN NCBI_TaxID=2095;
RP SEQUENCE FROM N.A.
RC STRAIN=Nelspruit;
RA Planet P., Jagoueix S., Bove J.M., Garnier M.;
RT "Detection and characterization of the African Citrus Greening
  Liberibacter by amplification, cloning and sequencing of the rplKAL-
  rpoBC operon.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
  OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
  SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
  (RNA)(N).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
  ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
  BETA' CHAIN.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL; U09675; AAA19557.1; -
CC InterPro: IPR001572; RNA_pol_B.
CC Pfam; PF00562; RNA_pol_B; 1.
CC PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
CC Transferase; Transcription; DNA-directed RNA polymerase.
FT NON TER 146 146
SQ SEQUENCE 146 AA; 16731 MW; 815D6EDD68FD8943 CRC64;

Query Match 53.5%; Score 38; DB 1; Length 146;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKNRMRK 10
DB 10 CVQNSRGARK 19

RESULT 12
Y125 MYCCA STANDARD; PRT; 267 AA.
AC P33661;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mycoplasma capricolum
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Entomoplasmataceae.

```

```

OX NCBI_TaxID=2095;
RN NCBI_TaxID=2095;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27343 / KID;
RX MEDLINE=96059641; PubMed=7476192;
RA Bork P., Ouzounis C., Casari G., Schneider R., Sander C.,
  Dolan M., Gilbert W., Gillevet P.M.;
RT "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
  its physiology.";
RL Mol. Microbiol. 16:955-967(1995).
CC -!- SIMILARITY: BELONGS TO THE COF/YEHA/YIDA/YIGL (E. COLL) / YCSE/YXEH
  (B.SUBTILIS) FAMILY.
CC
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CC
CC EMBL; Z33006; CAA83689.1; -
CC InterPro: IPR001454; Hlgnase/hydrilase.
CC InterPro: IPR000150; Hypothet_cof.
CC Pfam; PF00702; Hydrolase; 1.
CC PROSITE; PS01228; COF_1; 1.
CC PROSITE; PS01229; COF_2; 1.
CC Hypothetical protein.
FT NON TER 267 267
SQ SEQUENCE 267 AA; 30425 MW; D5912DD5B39A8451 CRC64;

Query Match 53.5%; Score 38; DB 1; Length 267;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKNRMRK 12
DB 158 CFQWKNRMRK 169

RESULT 13
VIF SIVS4 STANDARD; PRT; 214 AA.
AC P12505;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Virion infectivity factor (SOR protein) (Q protein).
GN VIF.
OS Simian immunodeficiency virus (F236/smH4 isolate) (sooty mangabey).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11737;
RN NCBI_TaxID=2095;
RP SEQUENCE FROM N.A.
RX MEDLINE=89262053; PubMed=2786147;
RA Hirsch V.M., Olmstead R.A., Murphy-Corb M., Purcell R.H.,
  Johnson P.R.;
RT "An African primate lentivirus (SIVem) closely related to HIV-2.";
RL Nature 339:389-392(1989). VIRUS INFECTIVITY.
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC
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CC
CC EMBL; X14307; CAA32484.1; -
CC HIV; S07989; S07989.
CC InterPro: IPR000475; Viral_infect.

```

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DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFECT.
DR PRODOM; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 214 AA; 25140 MW; 9BCE3884EC454BF3D CRC64;

Query Match 52.1%; Score 37; DB 1; Length 214;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 3 QWRNRK 10
|:|:|:|:|
Db 170 QWRNRK 177

RESULT 14
YNR2_CABEL STANDARD; PRT; 783 AA.
AC Q21986;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein R13G10.2 in chromosome III.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gardner A.E.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Durbin R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: FAD (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
CC
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CC
CC EMBL; Z35602; CAA84671.2; -.
CC WormPep; R13G10.2; CE25086.
CC InterPro; IPR002937; Amino_oxidase.
CC Pfam; PF01593; Amino_oxidase; 1.
KW Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
FT NP_BIND 311 366 FAD (ADP PART) (POTENTIAL).
SQ SEQUENCE 783 AA; 88799 MW; 8D087E96464DC908 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 783;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWKRNRKVR 12
|:|:|:|:|
Db 540 CIDWGRDRKVR 551

RESULT 15
1A34_HUMAN STANDARD; PRT; 365 AA.
AC P30453; P30454;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, AW-34(A-10) alpha chain

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DE GN HLA-A OR HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*3401/A*3402).
RX MEDLINE=93056508; PubMed=1431115;
RA Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
RA Martell R.W., du Toit E.D., Parham P.;
RT "Distinctive HLA-A,B antigens of black populations formed by
RT interallelic conversion."
RL J. Immunol. 149:3411-3415(1992).
RN [2]
RP SEQUENCE FROM N.A. (A*3401/A*3402).
RX MEDLINE=9323211; PubMed=8475492;
RA Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
RA du Toit E.D., Parham P.;
RT "Structural diversity in the HLA-A10 family of alleles: correlations
RT with serology."
RL Tissue Antigens 41:72-80(1993).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -1- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401
CC (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
CC A*3401.
CC
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CC
CC EMBL; X61704; CAA43873.1; -.
CC EMBL; X61705; CAA43874.1; -.
CC PIR; S16767; S16767.
CC PIR; S16771; S16771.
CC HSP; O19673; 1HSB.
CC MIM; 142800; -.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_C1.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00129; MHC_I; 1.
CC PRODOM; PD000050; MHC_I; 1.
CC SMART; SM00407; IG1; 1.
CC PROSITE; PS00250; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT AW-34 (A-10) ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT VARIANT 3 3 I -> V (IN A*3402).
FT VARIANT 90 90 K -> N (IN A*3402).
FT VARIANT 121 121 R -> I (IN A*3402).
FT VARIANT 121 121 /FTID=VAR_004381.
FT /FTID=VAR_004381.

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FT VARIANT 129 129 P -> S (IN A*3402).
FT FTID=VAR 004382.
FT VARIANT 138 138 Q -> R (IN A*3402).
FT FTID=VAR 004383.
FT VARIANT 180 180 W -> L (IN A*3402).
FT FTID=VAR 004384.
FT VARIANT 312 312 L -> I (IN A*3402).
FT FTID=VAR 004385.
SQ SEQUENCE 365 AA; 41055 MW; 063BF63E656E01F6 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 365;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WKRNRKVR 12
Db 84 WDRNRKVK 92

```

Search completed: February 21, 2003, 07:51:39
 Job time : 6.2093 secs

GenCore version 5.1.3
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PM protein - protein search, using sw model

Run on: February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
(without alignments)
114.078 Million cell updates/sec

Title: US-09-743-107B-92

Perfect score: 71

Sequence: 1 CFQWKNMRKV 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	DB ID	Description
1	62	87.3	711	4	Q8TCD2 homo sapien
2	58	81.7	38	4	Q9UCY5 homo sapien
3	47	66.2	33	6	Q9TR80 ovis ariet
4	45	63.4	275	5	Q93780 caenorhabdi
5	41	57.7	62	16	Q8R9U1
6	41	57.7	205	16	Q986A0 rhizobium l
7	41	57.7	206	16	Q8UHC2 agrobacteri
8	41	57.7	206	16	Q92RH8 rhizobium m
9	41	57.7	208	16	Q8YFK3 bruceella me
10	41	57.7	511	16	Q8Z462 salmonella
11	40	56.3	81	15	Q90863 human immun
12	40	56.3	148	10	Q9XHP1
13	40	56.3	274	4	Q96M21
14	40	56.3	584	17	Q9HPA3
15	39	54.9	273	2	Q31090 rhizobium l
16	39	54.9	279	16	Q8XSE2 ralstonia s

17	39	54.9	447	5	017549	017549 caenorhabdi
18	39	54.9	550	11	Q9JZJ5	Q9JZJ5 mus musculu
19	39	54.9	759	16	Q9Z955	Q9Z955 chlamydia p
20	39	54.9	864	5	062582	062582 encephalito
21	39	54.9	864	5	Q8SRG3	Q8SRG3 encephalito
22	39	54.9	864	5	Q8SQI6	Q8SQI6 encephalito
23	38	53.5	81	15	Q90884	Q90884 human immun
24	38	53.5	91	15	Q77855	Q77855 human immun
25	38	53.5	105	10	Q9XFD5	Q9XFD5 oryza sativ
26	38	53.5	207	10	Q9SML1	Q9SML1 cicor ariet
27	38	53.5	240	10	Q9SML2	Q9SML2 cicor ariet
28	38	53.5	253	12	Q8541	Q8541 horseradish
29	38	53.5	238	16	Q8YP77	Q8YP77 horseradish
30	38	53.5	306	4	Q8TAX2	Q8TAX2 homo sapien
31	38	53.5	329	2	Q9F7Y4	Q9F7Y4 salmonella
32	38	53.5	341	11	Q8R2A4	Q8R2A4 mus musculu
33	38	53.5	372	10	Q81653	Q81653 hemerocalli
34	38	53.5	393	10	Q9ZTP0	Q9ZTP0 oryza sativ
35	38	53.5	393	16	Q25611	Q25611 helicobacte
36	38	53.5	402	10	Q9ZRH8	Q9ZRH8 oryza sativ
37	38	53.5	466	4	Q9NUS2	Q9NUS2 homo sapien
38	38	53.5	489	16	P96223	P96223 mycobacteri
39	38	53.5	499	10	Q9XFX1	Q9XFX1 cicor ariet
40	38	53.5	560	10	Q9FTT0	Q9FTT0 oryza sativ
41	38	53.5	570	10	Q8S487	Q8S487 zea mays (m
42	38	53.5	583	10	Q81437	Q81437 arabidopsis
43	38	53.5	662	12	Q9QU30	Q9QU30 ttv-like mi
44	38	53.5	666	5	Q9W1D5	Q9W1D5 drosophila
45	38	53.5	866	10	Q9FHI9	Q9FHI9 arabidopsis

ALIGNMENTS

RESULT 1

Q8TCD2 ID Q8TCD2 PRELIMINARY; PRT; 711 AA.
 AC Q8TCD2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Lactotransferrin.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PROSTATE;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC023347; AAH23347.1;
 SQ SEQUENCE 711 AA; 78327 MW; 1B9C7BE097C45FAF CRC64;

Query Match 87.3%; Score 62; DB 4; Length 711;
 Best Local Similarity 90.9%; Pred. No. 0.0074;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFQWKNMRKV 11
 Db 39 CFQWKNMRKV 49

RESULT 2

Q9UCY5 ID Q9UCY5 PRELIMINARY; PRT; 38 AA.
 AC Q9UCY5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Lactoferrin homolog (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96081613; PubMed=8551695;
 RA Sato I.;
 RT "Characterization of the 84-kDa protein with ABH activity in human
 seminal plasma.";
 RL Jpn. J. Legal Med. 49:281-293 (1995).
 DR HSP; P02788; IBLX.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 38 AA; 4459 MW; 0402F49035EBDDDEB CRC64;

Query Match 81.7%; Score 58; DB 4; Length 38;
 Best Local Similarity 90.9%; Pred. No. 0.0019;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FQWKNRMRKV 12
 |||:|||||
 Db 21 FQWKNRMRKV 31

RESULT 3
 Q9TR80 PRELIMINARY; PRT; 33 AA.
 AC Q9TR80;
 DT 01-WAY-2000 (TRENBLrel. 13, Created)
 DT 01-WAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95127729; PubMed=7827104;
 RA Qian Z.Y., Joiles P., Migliore-Sancour D., Fiat A.M.;
 RL Biochim. Biophys. Acta 1243:25-32 (1995).
 DR HSP; O77698; ICE2.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 66.2%; Score 47; DB 6; Length 33;
 Best Local Similarity 54.5%; Pred. No. 0.16;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKNRMRKV 11
 |||:|
 Db 19 CYQWQKMRKL 29

RESULT 4
 Q93780 PRELIMINARY; PRT; 275 AA.
 AC Q93780;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE F53H4.4 protein.
 GN F53H4.4
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dobson R.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=95069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018 (1998).
 DR EMBL; Z81089; CAB03137.1; -;
 SQ SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;

Query Match 63.4%; Score 45; DB 5; Length 275;
 Best Local Similarity 72.7%; Pred. No. 3.1;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQWKNRMRKV 12
 |||:|||||
 Db 262 FQWKNRMRKV 272

RESULT 5
 Q8R9U1 PRELIMINARY; PRT; 62 AA.
 AC Q8R9U1;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Ribosomal protein L28.
 GN RPB OR TWE1495.
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4T / JCM11007;
 RX MEDLINE=21992816; PubMed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RA "A complete sequence of T. tengcongensis genome.";
 RT Genome Res. 12:689-700 (2002).
 RL EMBL; AE013107; AAM24713.1; -;
 KW Complete proteome.
 SQ SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;

Query Match 57.7%; Score 41; DB 16; Length 62;
 Best Local Similarity 70.0%; Pred. No. 3.6;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWKNRMRKV 12
 |||:|
 Db 27 RWKPNRKR 36

RESULT 6
 Q986A0 PRELIMINARY; PRT; 205 AA.
 AC Q986A0;
 DT 01-OCT-2001 (TRENBLrel. 18, Created)
 DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Pyridoxamine 5'-phosphate oxidase.
 GN ML7454.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=391;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214969;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

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RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RT Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RL Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003011; BAB53553.1; -.
DR InterPro; IPR000659; Pyridox_oxidase.
DR Pfam; PF01243; Pyridox_oxidase; 1.
DR ProDom; PD008312; Pyridox_oxidase; 1.
DR TIGRfams; TIGR00558; pdxH; 1.
DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
DR Complete proteome.
SQ SEQUENCE 205 AA; 23300 MW; 0BAD54CD312327EA CRC64;

Query Match 57.7%; Score 41; DB 16; Length 205;
Best Local Similarity 58.3%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

2Y 1 CFQWRNMRKVR 12
   |||||
Db 88 CFHWKSLRRQVR 99

RESULT 7
2D Q8UHC2 PRELIMINARY; PRT; 206 AA.
2C Q8UHC2;
2T 01-JUN-2002 (TrEMBLrel. 21, Created)
2T 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
2T 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
2E Pyridoxamine 5'-phosphate oxidase.
2S PDHX OR ATU0760 OR AGR C.1381.
2S Agrobacterium tumefaciens (strain C58 / ATCC 33970).
2C Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
2C Rhizobiaceae; Rhizobium.
2X NCBI_TaxID=176299;
2N [1]
2P SEQUENCE FROM N.A.
2A MEDLINE=21608550; PubMed=11743193;
2A Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
2A Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
2A Chen Y., Paulsen I.T., Elesen J.A., Karp P.D., Bovee D. Sr.,
2A Chapman P., Clendenning J., Decherage G., Gillet W., Grant C.,
2A Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
2A Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
2A Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
2A Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
2A Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
2A Nester E.W.;
2T "The genome of the natural genetic engineer Agrobacterium tumefaciens
CS8.";
2L Science 294:2317-2323(2001).
2N [2]
2P SEQUENCE FROM N.A.
2A MEDLINE=21608551; PubMed=11743194;
2A Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
2A Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
2A Houniel K., Gordon J., Vaudin M., Farchouk O., Epp A., Liu F.,
2A Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
2A Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
2A Cielo C., Slater S.;
2T "Genome sequence of the plant pathogen and biotechnology agent
2T Agrobacterium tumefaciens C58.";
2L Science 294:2323-2328(2001).
2R EMBL; AEO09043; AAL41776.1; -.
2R EMBL; AEO08009; AAK8569.1; -.
2W Complete proteome.
2Q SEQUENCE 206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;

Query Match 57.7%; Score 41; DB 16; Length 206;
Best Local Similarity 58.3%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 1 CFQWRNMRKVR 12
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Db 88 CFHWKSLRRQVR 99

RESULT 8
Q2RHH8 PRELIMINARY; PRT; 206 AA.
ID Q2RHH8;
AC Q2RHH8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
DE (EC 1.4.3.5).
DN PDHX OR R00895 OR SMC00069.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
2N [1]
2P SEQUENCE FROM N.A.
2C STRAIN=1021;
2C MEDLINE=21396507; PubMed=11481430;
2A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
2A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
2A Godrie T., Coffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
2A Pohl T., Portetelle D., Fuehler A., Fumelle B., Ramsperger U.,
2A Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F.;
2T "Analysis of the chromosome sequence of the legume symbiont
2T Sinorhizobium meliloti strain 1021.";
2L Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
2R EMBL; AL591785; CAC45467.1; -.
2R InterPro; IPR000659; Pyridox_oxidase.
2R Pfam; PF01243; Pyridox_oxidase; 1.
2R ProDom; PD006312; Pyridox_oxidase; 1.
2R TIGRfams; TIGR00558; pdxH; 1.
2R PROSITE; PS01064; PYRIDOX_OXIDASE; UNKNOWN_1.
2K Oxidoreductase; Complete proteome.
2Q SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;

Query Match 57.7%; Score 41; DB 16; Length 206;
Best Local Similarity 58.3%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWRNMRKVR 12
   |||||
Db 88 CFHWKSLRRQVR 99

RESULT 9
Q8YFK3 PRELIMINARY; PRT; 208 AA.
ID Q8YFK3;
AC Q8YFK3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5).
GN BMEI1517.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
2N [1]
2P SEQUENCE FROM N.A.
2C STRAIN=16M / ATCC 23456 / BIOTYPE 1;
2C MEDLINE=20020109; PubMed=11756688;
2A DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Muier C., Los T.,
2A Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
2A Jablonksi L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
2A Seikov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
2A Haselkorn R., Kyriades N., Overbeek R.;
2T "The genome sequence of the facultative intracellular pathogen
2T Brucella melitensis.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009587; AL52698.1; -.
DR InterPro; IPR000659; Pyridox oxidase.
DR Pfam; PF01243; Pyridox oxidase; 1.
DR ProDom; PD006312; Pyridox oxidase; 1.
DR TIGRfams; TIGR00558; pdxh; 1.
DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 208 AA; 23866 MW; CB1F50BC9612DE28 CRC64;

Query Match 57.7%; Score 41; DB 16; Length 208;
Best Local Similarity 58.3%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKNRNVKVR 12
DB 90 CFHWKSLRRQVR 101

RESULT 10
O8Z462 PRELIMINARY; PRT; 511 AA.
AC Q8Z462;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein STY3070.
GN STY3070
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OC NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi Ct18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627276; CAD06049.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 511 AA; 58126 MW; E2DDDL24E10D178B CRC64;

Query Match 57.7%; Score 41; DB 16; Length 511;
Best Local Similarity 58.3%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWKNRNVKVR 12
DB 350 CFWDNKNKAKVR 361

RESULT 11
O90863 PRELIMINARY; PRT; 81 AA.
AC O90863;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein gp120 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=NJS182;
RA Brandful J.A.M., Ampofo W.K., Janssens W., Adu-Sarkodie Y.,
RA Agyeyei F., Anyomi F., Aidoo S., Barnor J.S., Yamamoto N.,
RA Ishikawa K., Sata T., Kurata T.;
RT "Genetic and phylogenetic analysis of HIV-1 strains from Southern
RT Ghana.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225659; CAA12541.1; -.
DR InterPro; IPR000777; GPI20.
DR Pfam; PF00516; GPI20; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9138 MW; 2D43DCD554295572 CRC64;

Query Match 56.3%; Score 40; DB 15; Length 81;
Best Local Similarity 66.7%; Pred. No. 7.1;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWKNRNVKVR 11
DB 69 EWNENRNVKVR 77

RESULT 12
O9XHP1 PRELIMINARY; PRT; 148 AA.
AC O9XHP1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OC NCBI_TaxID=4182;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TAINAN 1;
RC MEDLINE=20074970; PubMed=10606554;
RX Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
RA "Molecular cloning of 11S globulin and 2S albumin, the two major seed
RT storage proteins in sesame.";
RL J. Agric. Food Chem. 47:4932-4938(1999).
DR EMBL; AF091841; AAD42943.1; -.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR000617; Napin.
DR InterPro; IPR001768; Try/amy1 inhbt.
DR Pfam; PF00234; tryp_alpha_amy1; 1.
DR PRINTS; PR00496; NAPIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 56.3%; Score 40; DB 10; Length 148;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKNRNVKVR 9
DB 54 CMQWRSNR 62

RESULT 13
O96M21 PRELIMINARY; PRT; 274 AA.
AC O96M21;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CDNA FLJ32891 fis, clone TEST12004929.
OS Homo sapiens (Human).

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DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
 RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahari K., Masuko Y., Nagai K., Isogai T.,
 RA "NEDO human cDNA sequencing project."
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK057453; BAB71493.1; -.
 RQ SEQUENCE 274 AA; 30083 MW; 1DD34654D4135B2F CRC64;

Query Match 56.3%; Score 40; DB 4; Length 274;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Y 1 CFQWRNMRKVR 12
 |||:|:|:
 b 66 CFQWRNMRKVR 77

RESULT 14
 J9HPA3 PRELIMINARY; PRT; 584 AA.
 AC Q9HPA3;
 IC Q9HPA3;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Vngl732C.
 EN Vngl732C.
 CS Halobacterium sp. (strain NRC-1).
 CC Archaea; Euryarchaeota; Halobacteriales;
 CC Halobacteriaceae; Halobacterium.
 CX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Fohlischroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Oner A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE005078; AAG19967.1; -.
 DR InterPro; IPR001646; Septide_repeat.
 DR InterPro; IPR001622; K-channel_pore.
 DR Pfam; PF00805; Pentapeptide; 2.
 KW Complete proteome.
 RQ SEQUENCE 584 AA; 65151 MW; 21BF5D5F0486CCC6 CRC64;

Query Match 56.3%; Score 40; DB 17; Length 584;
 Best Local Similarity 41.7%; Pred. No. 54;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Y 1 CFQWRNMRKVR 12
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 b 445 CFQWRNMRKVR 456

RESULT 15
 J31090 PRELIMINARY; PRT; 273 AA.
 ID O31090
 AC O31090;

DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
 DE Hypothetical 31.0 kDa protein.
 OS Rhizobium leguminosarum (biovar viciae).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 CX NCBI_TaxID=387;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF39;
 RA Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N.;
 RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF39;
 RX MEDLINE=99113394; PubMed=9914965;
 RA Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G.,
 RA Ksenzenko V.N.;
 RT "Structural and functional organization of the exopolysaccharide
 biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39."
 RL Mol. Biol. (Mosk) 32:797-804(1998).
 DR EMBL; AF028810; AAB88991.1; -.
 KW Hypothetical protein.
 RQ SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;

Query Match 54.9%; Score 39; DB 2; Length 273;
 Best Local Similarity 50.0%; Pred. No. 37;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Y 3 QWRNMRKVR 12
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 b 245 RWRNMRKVR 254

Search completed: February 21, 2003, 08:00:45
 Job time : 22.6744 secs

GenCore version 5.1.3
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Ⓜ protein - protein search, using sw model

run on: February 21, 2003, 07:37:21 ; Search time 28.093 Seconds
(without alignments)
56.918 Million cell updates/sec

Title: US-09-743-107B-93

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Scoring table: BLOSUM62

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length DB	ID	Description
1	69	100.0	12	21	AAV78093 Human lactoferrin
2	65	94.2	12	21	AAV78074 Human lactoferrin
3	63	91.3	12	21	AAV78091 Human lactoferrin
4	63	91.3	12	21	AAV78092 Human lactoferrin
5	61	88.4	12	21	AAV78089 Human lactoferrin
6	61	88.4	12	21	AAV78090 Human lactoferrin
7	60	87.0	12	21	AAV78086 Human lactoferrin
8	59	85.5	12	21	AAV78038 Human lactoferrin
9	59	85.5	12	21	AAV78046 Human lactoferrin
10	59	85.5	12	21	AAV78047 Human lactoferrin

11	59	85.5	12	21	AAV78084 Human lactoferrin
12	59	85.5	12	21	AAV78095 Human lactoferrin
13	59	85.5	13	21	AAV78037 Human lactoferrin
14	59	85.5	13	21	AAV78048 Human lactoferrin
15	59	85.5	13	21	AAV78049 Human lactoferrin
16	59	85.5	14	21	AAV78036 Human lactoferrin
17	59	85.5	14	21	AAV78050 Human lactoferrin
18	59	85.5	14	21	AAV78051 Human lactoferrin
19	59	85.5	15	17	AAV78055 Peptide for anti-u
20	59	85.5	15	21	AAV78035 Human lactoferrin
21	59	85.5	15	21	AAV78062 Human lactoferrin
22	59	85.5	15	21	AAV78063 Human lactoferrin
23	59	85.5	16	21	AAV78031 Human lactoferrin
24	59	85.5	16	21	AAV78064 Human lactoferrin
25	59	85.5	16	21	AAV78065 Human lactoferrin
26	59	85.5	17	21	AAV78034 Human lactoferrin
27	59	85.5	17	21	AAV78066 Human lactoferrin
28	59	85.5	17	21	AAV78067 Human lactoferrin
29	59	85.5	18	15	AAV78032 Human lactoferrin
30	59	85.5	18	17	AAV78033 Human lactoferrin
31	59	85.5	18	21	AAV78033 Human lactoferrin
32	59	85.5	19	21	AAV78032 Human lactoferrin
33	59	85.5	19	21	AAV78032 Human lactoferrin
34	59	85.5	20	13	AAV78032 Human lactoferrin
35	59	85.5	20	14	AAV78032 Human lactoferrin
36	59	85.5	20	15	AAV78032 Human lactoferrin
37	59	85.5	20	15	AAV78032 Human lactoferrin
38	59	85.5	20	15	AAV78032 Human lactoferrin
39	59	85.5	20	15	AAV78032 Human lactoferrin
40	59	85.5	20	16	AAV78032 Human lactoferrin
41	59	85.5	20	16	AAV78032 Human lactoferrin
42	59	85.5	20	16	AAV78032 Human lactoferrin
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44	59	85.5	20	16	AAV78032 Human lactoferrin
45	59	85.5	20	17	AAV78032 Human lactoferrin

ALIGNMENTS

RESULT 1

AAV78093
ID AAV78093 standard; Peptide; 12 AA.
XX AAV78093;
XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:93.
XX Human lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
XX 13-JAN-2000.
XX 06-JUL-1999; 99WO-SE01230.
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 22; Page 38; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX
XX SQ Sequence 12 AA;
Query Match 100.0%; Score 69; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWKRAMRKVR 12
DB 1 CFQWKRAMRKVR 12
|||||

RESULT 2
AAY78074
ID AAY78074 standard; Peptide; 12 AA.
XX
AC AAY78074;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:74.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-S01230.
XX
XX 06-JUL-1998; 98SE-0002441.
XX
XX 17-JUL-1998; 98SE-0002562.
XX
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 22; Page 35; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX
XX SQ Sequence 12 AA;
Query Match 94.2%; Score 65; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00019;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFQWKRAMRKVR 12
DB 1 CFQWKRAMRKVR 12
|||||

RESULT 3
AAY78091
ID AAY78091 standard; Peptide; 12 AA.
XX
AC AAY78091;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:91.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
XX
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-S01230.
XX
XX 06-JUL-1998; 98SE-0002441.
XX
XX 17-JUL-1998; 98SE-0002562.
XX
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX Claim 22; Page 38; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

XX fungicidal and bactericidal and may also be used as preservatives.
 XX Even though native human lactoferrin have been shown to have desired
 XX anti-inflammatory anti-infectious and anti-tumoural properties they
 XX cannot be used clinically on a broad basis because of high production
 XX costs. Therefore, provision of peptides based on lactoferrin would
 XX enable them to be used for the same purposes as lactoferrin at lower
 XX cost.

QY Sequence 12 AA;
 Query Match 91.3%; Score 63; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00042;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKRAMRKVR 12
 DB 1 CFQWKRAMRKVR 12

RESULT 4
 AAY78092
 ID AAY78092 standard; Peptide; 12 AA.

XX AAY78092;
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:92.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX urinary tract infection; colitis; Candida infection; fungicidal;
 XX bactericidal; preservative.

XX Homo sapiens.
 XX Synthetic.

XX WO200001730-A1.
 XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

XX inflammations and tumors and for use in infant formula food -

XX Claim 22; Page 38; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through
 XX binding to specific lactoferrin receptors and are then transported
 XX through the circulation. A medicinal product of the peptide or fragment
 XX can be used for treating and/or prevention of infections (such as
 XX urinary tract infections, colitis, and Candida infection on a mucosal
 XX membrane), inflammations and/or tumours. The peptides can also be used
 XX in food stuffs such as infant formula food. The peptides are also
 XX fungicidal and bactericidal and may also be used as preservatives.
 XX Even though native human lactoferrin have been shown to have desired
 XX anti-inflammatory anti-infectious and anti-tumoural properties they
 XX cannot be used clinically on a broad basis because of high production
 XX costs. Therefore, provision of peptides based on lactoferrin would
 XX enable them to be used for the same purposes as lactoferrin at lower
 XX cost.

XX SQ Sequence 12 AA;
 Query Match 91.3%; Score 63; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00042;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKRAMRKVR 12
 DB 1 CFQWKRAMRKVR 12

RESULT 5
 AAY78089
 ID AAY78089 standard; Peptide; 12 AA.

XX AC
 XX AAY78089;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:89.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX urinary tract infection; colitis; Candida infection; fungicidal;
 XX bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,

XX inflammations and tumors and for use in infant formula food -

XX Claim 22; Page 37; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through
 XX binding to specific lactoferrin receptors and are then transported
 XX through the circulation. A medicinal product of the peptide or fragment
 XX can be used for treating and/or prevention of infections (such as
 XX urinary tract infections, colitis, and Candida infection on a mucosal
 XX membrane), inflammations and/or tumours. The peptides can also be used
 XX in food stuffs such as infant formula food. The peptides are also
 XX fungicidal and bactericidal and may also be used as preservatives.
 XX Even though native human lactoferrin have been shown to have desired
 XX anti-inflammatory anti-infectious and anti-tumoural properties they
 XX cannot be used clinically on a broad basis because of high production
 XX costs. Therefore, provision of peptides based on lactoferrin would
 XX enable them to be used for the same purposes as lactoferrin at lower
 XX cost.

XX SQ Sequence 12 AA;

Query Match 88.4%; Score 61; DB 21; Length 12;

Best Local Similarity 83.3%; Pred. No. 0.0009;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2y 1 CFQWXRMRKVR 12
 ||||:|||||
 3b 1 CFQWXRMRKVR 12

RESULT 6

AA78090
 ID AA78090 standard; Peptide; 12 AA.

XX AC AA78090;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:90.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-S001230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food

XX PS Claim 22; Page 37; 102pp; English.

XX CC AA78001 to AA78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane, inflammations, colitis, and Candida infection on a mucosal
 CC in food stuffs such as infant formula food. The peptides can also be used
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 88.4%; Score 61; DB 21; Length 12;
 Best Local Similarity 83.3%; Pred. No. 0.0009;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWXRMRKVR 12

DB 1 CFQWXRMRKVR 12

RESULT 7

AA78086

ID AA78086 standard; Peptide; 12 AA.

XX AC AA78086;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:86.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-S001230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food

XX PS Claim 22; Page 36; 102pp; English.

XX CC AA78001 to AA78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane, inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides can also be used
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 87.0%; Score 60; DB 21; Length 12;
 Best Local Similarity 83.3%; Pred. No. 0.0013;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWXRMRKVR 12

DB 1 CFQWXRMRKVR 12

RESULT 8

AA78038

ID AA78038 standard; Peptide; 12 AA.

XX AC AA78038;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:38.

CX Human; lactoferrin; modification; infection; inflammation; tumour;
 CW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 CW urinary tract infection; colitis; Candida infection; fungicidal;
 CW bactericidal; preservative.
 XS Homo sapiens.
 XS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 XX 17-JUL-1998; 98SE-0002562.
 XX 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -
 XX Claim 12; Page 70; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through
 XX binding to specific lactoferrin receptors and are then transported
 XX through the circulation. A medicinal product of the peptide or fragment
 XX can be used for treating and/or prevention of infections (such as
 XX urinary tract infections, colitis, and Candida infection on a mucosal
 XX membrane), inflammations and/or tumours. The peptides can also be used
 XX in food stuffs such as infant formula food. The peptides are also
 XX fungicidal and bactericidal and may also be used as preservatives.
 XX Even though native human lactoferrin have been shown to have desired
 XX anti-inflammatory anti-infectious and anti-tumoural properties they
 XX cannot be used clinically on a broad basis because of high production
 XX costs. Therefore, provision of peptides based on lactoferrin would
 XX enable them to be used for the same purposes as lactoferrin at lower
 XX cost.
 XX Sequence 12 AA;
 XX Query Match 85.5%; Score 59; DB 21; Length 12;
 XX Best Local Similarity 83.3%; Pred. No. 0.002; 1; Indels 0; Gaps 0;
 XX Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 YY 1 CFQWKRAVRKVR 12
 YY ||||:||||
 Yb 1 CFQWQRNRKVR 12
 Yb ||||:||||
 RESULT 9
 XAY78046
 XD AAY78046 standard; Peptide; 12 AA.
 XC AAY78046;
 CX 25-APR-2000 (first entry)
 CX Human lactoferrin derived peptide SEQ ID NO:46.
 CX Human; lactoferrin; modification; infection; inflammation; tumour;
 CX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 CX urinary tract infection; colitis; Candida infection; fungicidal;
 CX bactericidal; preservative.
 XS Homo sapiens.

OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 XX 17-JUL-1998; 98SE-0002562.
 XX 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 35; 102pp; English.
 XX AAY78001 to AAY78100 represent peptides having sequences based on human
 XX lactoferrin. The peptides are taken up in the intestine through
 XX binding to specific lactoferrin receptors and are then transported
 XX through the circulation. A medicinal product of the peptide or fragment
 XX can be used for treating and/or prevention of infections (such as
 XX urinary tract infections, colitis, and Candida infection on a mucosal
 XX membrane), inflammations and/or tumours. The peptides can also be used
 XX in food stuffs such as infant formula food. The peptides are also
 XX fungicidal and bactericidal and may also be used as preservatives.
 XX Even though native human lactoferrin have been shown to have desired
 XX anti-inflammatory anti-infectious and anti-tumoural properties they
 XX cannot be used clinically on a broad basis because of high production
 XX costs. Therefore, provision of peptides based on lactoferrin would
 XX enable them to be used for the same purposes as lactoferrin at lower
 XX cost.
 XX Sequence 12 AA;
 XX Query Match 85.5%; Score 59; DB 21; Length 12;
 XX Best Local Similarity 83.3%; Pred. No. 0.002; 1; Indels 0; Gaps 0;
 XX Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CFQWKRAVRKVR 12
 Qy ||||:||||
 Db 1 CFQWQRNRKVR 12
 Db ||||:||||
 RESULT 10
 AAY78047
 ID AAY78047 standard; Peptide; 12 AA.
 XX AAY78047;
 XX AC AAY78047;
 XX 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:47.
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX urinary tract infection; colitis; Candida infection; fungicidal;
 XX bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200001730-A1.
 XX 13-JAN-2000.
 XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food
 XX Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;

Query Match 85.5%; Score 59; DB 21; Length 12;
 Best Local Similarity 83.3%; Pred. No. 0.002;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKRAMRKVR 12
 DB 1 CFQWQRMNRKVR 12

RESULT 11
 AAY78084
 ID AAY78084 standard; Peptide; 12 AA.

XX AAY78084;
 AC
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:84.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food
 XX Claim 22; Page 36; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;

Query Match 85.5%; Score 59; DB 21; Length 12;
 Best Local Similarity 83.3%; Pred. No. 0.002;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKRAMRKVR 12
 DB 1 CFQWQRMNRKVR 12

RESULT 12
 AAY78095
 ID AAY78095 standard; Peptide; 12 AA.

XX AAY78095;

AC
 DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:95.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food
 XX

Claim 22; Page 38; 102pp; English.

AA78001 to AA78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.

Sequence 12 AA;

Query Match 85.5%; Score 59; DB 21; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.002;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 CFQWKRMRKVR 12

1 CFQWKRMRKVR 12

RESULT 13

AA78037

AA78037 standard; Peptide; 13 AA.

AA78037;

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:37.

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens.

Synthetic.

WO200001730-A1.

13-JAN-2000.

06-JUL-1999; 99WO-SE01230.

06-JUL-1998; 98SE-0002441.

17-JUL-1998; 98SE-0002562.

29-DEC-1998; 98SE-0004614.

(ASCI-) A+ SCI INVEST AB.

Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 12; Page 70; 102pp; English.

AA78001 to AA78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as

urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.

Sequence 13 AA;

Query Match 85.5%; Score 59; DB 21; Length 13;
Best Local Similarity 83.3%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 CFQWKRMRKVR 12

2 CFQWKRMRKVR 13

RESULT 14

AA78048

AA78048 standard; Peptide; 13 AA.

AA78048;

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:48.

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens.

Synthetic.

WO200001730-A1.

13-JAN-2000.

06-JUL-1999; 99WO-SE01230.

06-JUL-1998; 98SE-0002441.

17-JUL-1998; 98SE-0002562.

29-DEC-1998; 98SE-0004614.

(ASCI-) A+ SCI INVEST AB.

Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 15; Page 74; 102pp; English.

AA78001 to AA78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX Sequence 13 AA;

Query Match 85.5%; Score 59; DB 21; Length 13;
Best Local Similarity 83.3%; Pred. No. 0.0021;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWKRAMRKVR 12
Db 2 CFQWQRNWKVR 13

RESULT 15

AA78049

ID AAY78049 standard; Peptide; 13 AA.

AC AAY78049;

DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:49.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.

XX Homo sapiens.
DS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

PF 06-JUL-1999; 99WO-SE01230.

PR 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

PA (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

PI WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -

PS Claim 18; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX Sequence 13 AA;

Query Match 85.5%; Score 59; DB 21; Length 13;

Best Local Similarity 83.3%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CFQWKRAMRKVR 12
Db 2 CFQWQRNWKVR 13

Search completed: February 21, 2003, 07:56:44
Job time : 28.093 secs

GenCore version 5.1.3
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M protein - protein search, using sw model

un on: February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds
(without alignments)
39.537 Million cell updates/sec

title: US-09-743-107B-93
effect score: 69
equences: 1 CFQWRAMKVR 12

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 262574 seqs, 2942292 residues

total number of hits satisfying chosen parameters: 262574

inimum DB seq length: 0
aximum DB seq length: 200000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atadase : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pap:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pap:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pap:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pap:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pap:*
6: /cgn2_6/ptodata/1/1aa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Score	Query Match	Length	ID	Description
1	59	85.5	18	1	US-08-204-487-3	Sequence 3, Appli
2	59	85.5	18	2	US-08-485-948-8	Sequence 8, Appli
3	59	85.5	18	2	US-08-628-380-8	Sequence 8, Appli
4	59	85.5	18	2	US-08-475-055-8	Sequence 8, Appli
5	59	85.5	20	1	US-07-753-161A-3	Sequence 3, Appli
6	59	85.5	20	1	US-07-891-174-3	Sequence 3, Appli
7	59	85.5	20	1	US-08-204-487-1	Sequence 1, Appli
8	59	85.5	20	1	US-08-256-771-24	Sequence 24, Appli
9	59	85.5	20	1	US-08-256-771-25	Sequence 24, Appli
10	59	85.5	20	1	US-08-381-984-24	Sequence 24, Appli
11	59	85.5	20	1	US-08-381-984-25	Sequence 25, Appli
12	59	85.5	22	4	US-09-508-734-4	Sequence 4, Appli
13	59	85.5	24	4	US-09-508-734-6	Sequence 4, Appli
14	59	85.5	25	1	US-07-753-161A-10	Sequence 10, Appli
15	59	85.5	25	1	US-07-891-174-10	Sequence 10, Appli
16	59	85.5	25	4	US-08-204-487-7	Sequence 7, Appli
17	59	85.5	29	4	US-09-508-734-8	Sequence 8, Appli
18	59	85.5	36	1	US-07-753-161A-8	Sequence 8, Appli
19	59	85.5	36	1	US-07-891-174-8	Sequence 8, Appli
20	59	85.5	36	1	US-08-256-771-30	Sequence 30, Appli
21	59	85.5	36	1	US-08-381-984-29	Sequence 29, Appli
22	59	85.5	47	2	US-08-464-182A-6	Sequence 6, Appli
23	59	85.5	47	2	US-08-406-271-6	Sequence 6, Appli
24	59	85.5	50	2	US-08-693-274A-7	Sequence 7, Appli
25	59	85.5	52	4	US-09-017-043A-3	Sequence 3, Appli
26	59	85.5	53	2	US-08-464-182A-5	Sequence 5, Appli
27	59	85.5	53	2	US-08-406-271-5	Sequence 5, Appli

28	59	85.5	54	2	US-08-464-182A-2	Sequence 2, Appli
29	59	85.5	54	2	US-08-406-271-2	Sequence 2, Appli
30	59	85.5	694	3	US-08-724-586-2	Sequence 2, Appli
31	59	85.5	694	4	US-09-431-632-2	Sequence 2, Appli
32	59	85.5	694	4	US-09-932-190-2	Sequence 2, Appli
33	59	85.5	705	2	US-08-695-640-2	Sequence 2, Appli
34	59	85.5	708	2	US-08-695-640-4	Sequence 4, Appli
35	59	85.5	711	1	US-08-154-019-4	Sequence 4, Appli
36	59	85.5	711	1	US-08-461-333-4	Sequence 4, Appli
37	59	85.5	711	3	US-08-464-167-4	Sequence 4, Appli
38	59	85.5	711	3	US-09-158-313-4	Sequence 4, Appli
39	59	85.5	711	4	US-08-476-798-4	Sequence 4, Appli
40	56	81.2	711	1	US-08-145-681-2	Sequence 2, Appli
41	56	81.2	711	1	US-08-250-308-2	Sequence 2, Appli
42	56	81.2	711	1	US-08-453-703-2	Sequence 2, Appli
43	56	81.2	711	2	US-08-456-106-2	Sequence 2, Appli
44	56	81.2	711	3	US-08-456-108-2	Sequence 2, Appli
45	56	81.2	711	4	US-09-265-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGERAKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FUN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 85.5%; Score 59; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DY 1 CFQWKRAMRKVR 12
|||:|||||
Db 1 CFQWQNRMKVR 12
|||:|||||

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VIASSARA
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LP-Cl, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-485-948-8

Query Match 85.5%; Score 59; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DY 1 CFQWKRAMRKVR 12
|||:|||||
Db 1 CFQWQNRMKVR 12
|||:|||||

RESULT 3
US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VIASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LP-Cl, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-628-380-8

Query Match 85.5%; Score 59; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DY 1 CFQWKRAMRKVR 12
|||:|||||
Db 1 CFQWQNRMKVR 12
|||:|||||

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VIASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LP-Cl, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
S-08-475-055-8

Query Match 85.5%; Score 59; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

y 1 CFQWRMRKVR 12
|||:||||
b 1 CFQWRMRKVR 12

RESULT 5
S-07-755-161A-3
Sequence 3, Application US/07/755161A
Patent No: 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLES:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 85.5%; Score 59; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 0.0016; 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DY 1 CFQWKRMRKVR 12
DB 2 CFQWRNRKVR 13

RESULT 6
JS-07-891-174-3
Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 85.5%; Score 59; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0016; 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CFQWKRMRKVR 12
DB 2 CFQWRNRKVR 13

RESULT 7
US-08-204-487-1
Sequence 1, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGEKI
APPLICANT: DOSAKO, SHUN-ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESS: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
S-08-204-487-1

Query Match 85.5%; Score 59; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0016; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Y 1 CFQWKRAVRKVR 12
| | | | |
b 2 CFQWQRNKRKVR 13
| | | | |

RESULT 8
S-08-256-771-24
Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Manoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 85.5%; Score 59; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0016; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWKRAVRKVR 12
| | | | |
DB 2 CFQWQRNKRKVR 13
| | | | |

RESULT 9
US-08-256-771-25
Sequence 25, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Manoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25

Query Match 85.5%; Score 59; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0016; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWKRAVRKVR 12
| | | | |
DB 2 CFQWQRNKRKVR 13
| | | | |

RESULT 10
US-08-381-984-24

Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

Query Match 85.5%; Score 59; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 0.0016;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKRMRKVR 12

DB 2 CFQWQRMRKVR 13

RESULT 11

US-08-381-984-25

Sequence 25, Application US/08381984

Patent No. 5804555

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: ANTIOXIDANT

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

Query Match 85.5%; Score 59; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 0.0016;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKRMRKVR 12

DB 2 CFQWQRMRKVR 13

RESULT 12

US-09-508-734-4

Sequence 4, Application US/09508734

Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof

FILE REFERENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: PCT/KR99/00373

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: KR1998-29351

PRIOR FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4

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LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
3-09-508-734-4

Query Match      85.5%; Score 59; DB 4; Length 22;
Best Local Similarity 83.3%; Pred. No. 0.0018;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQWKRAMRKVR 12
   ||||| |||||
2 2 CFQWQRNMRKVR 13

RESULT 13
3-09-508-734-6
Sequence 6, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: KopatentIn 1.71
SEQ ID NO 6
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
3-09-508-734-6

Query Match      85.5%; Score 59; DB 4; Length 24;
Best Local Similarity 83.3%; Pred. No. 0.0019;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQWKRAMRKVR 12
   ||||| |||||
2 3 CFQWQRNMRKVR 14

RESULT 14
3-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLES:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10

Query Match      85.5%; Score 59; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 0.002;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKRAMRKVR 12
   ||||| |||||
DB 4 CFQWQRNMRKVR 15
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RESULT 15

US-07-891-174-10
Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: MAROTU TOMITA et al.
TITLE OF INVENTION: Antimicrobial peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 85.5%; Score 59; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 0.002;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWKGAMRKVR 12
DB 4 CFQWQRMNRKVR 15
Search completed: February 21, 2003, 08:04:27
Job time : 9.93023 secs

GenCore version 5.1.3
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M protein - protein search, using sw model

un on: February 21, 2003, 08:08:15 ; Search time 6.88372 Seconds
(without alignments)
54.162 Million cell updates/sec

file: US-09-743-107b-93

effect score: 69
sequence: 1 CFQWKRMRKVR 12

coring table: BLOSUM62
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searched: 156504 seqs, 31069816 residues

total number of hits satisfying chosen parameters: 156504

inimum DB seq length: 0

aximum DB seq length: 200000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PTCTUS_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	59	85.5	15	9	US-09-798-869-2
2	59	85.5	25	9	US-09-798-869-20
3	59	85.5	694	9	US-10-023-096-2
4	51	73.9	15	9	US-09-798-869-6
5	49	71.0	15	9	US-09-798-869-3
6	49	71.0	25	9	US-09-798-869-23
7	41	59.4	15	9	US-09-798-869-7
8	40	58.0	15	9	US-09-798-869-4
9	40	58.0	25	9	US-09-798-869-22
10	38	55.1	21	10	US-09-864-761-47985
11	37	53.6	15	9	US-09-798-869-8
12	37	53.6	15	9	US-09-798-869-29
13	37	53.6	15	9	US-09-798-869-30
14	37	53.6	489	9	US-09-888-320-2
15	36	52.2	86	9	US-09-738-626-5715
16	36	52.2	318	12	US-10-042-417-42
17	35	50.7	301	9	US-10-080-960-11
18	35	50.7	302	10	US-09-948-078-2
19	35	50.7	333	9	US-10-001-054-42

20	35	50.7	333	9	US-10-028-072-132	Sequence 132, App
21	35	50.7	333	9	US-10-121-049-132	Sequence 132, App
22	35	50.7	333	9	US-10-123-904-132	Sequence 132, App
23	35	50.7	333	9	US-10-140-470-132	Sequence 132, App
24	35	50.7	333	9	US-10-175-746-132	Sequence 132, App
25	35	50.7	333	9	US-10-176-918-132	Sequence 132, App
26	35	50.7	333	9	US-10-176-921-132	Sequence 132, App
27	35	50.7	333	9	US-10-137-865-132	Sequence 132, App
28	35	50.7	333	9	US-10-140-474-132	Sequence 132, App
29	35	50.7	351	10	US-09-853-625B-16	Sequence 16, Appl
30	34	49.3	138	9	US-10-013-379-14	Sequence 14, Appl
31	34	49.3	760	10	US-09-866-582-42	Sequence 42, Appl
32	33	47.8	95	10	US-09-764-864-1031	Sequence 1031, Ap
33	33	47.8	162	9	US-09-738-626-6604	Sequence 6604, Ap
34	33	47.8	238	9	US-09-986-480-182	Sequence 182, App
35	33	47.8	268	10	US-09-764-864-1172	Sequence 1172, Ap
36	33	47.8	411	10	US-09-764-864-899	Sequence 899, App
37	33	47.8	411	10	US-09-764-864-1346	Sequence 1346, Ap
38	33	47.8	414	9	US-09-978-295A-466	Sequence 466, App
39	33	47.8	414	9	US-09-764-857-12	Sequence 12, Appl
40	33	47.8	414	9	US-09-978-697-466	Sequence 466, App
41	33	47.8	414	9	US-09-978-192A-466	Sequence 466, App
42	33	47.8	414	9	US-09-993-832A-466	Sequence 466, App
43	33	47.8	414	9	US-09-978-139-466	Sequence 466, App
44	33	47.8	414	9	US-10-028-072-418	Sequence 418, App
45	33	47.8	414	9	US-10-121-049-418	Sequence 418, App

ALIGNMENTS

RESULT 1

US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798, 869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 85.5%; Score 59; DB 9; Length 15;
Best Local Similarity 83.3%; Pred No. 0.0047;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWKRMRKVR 12
| | | | | | | | | |
Db 3 CFQWQRNRKVR 14

RESULT 2

US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ RNSSON

APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match 85.5%; Score 59; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 0.00078;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWKRMKVR 12
DB 3 CFQWQNNMKVR 14

RESULT 3
US-10-023-096-2
Sequence 2, Application US/10023096
Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Krusel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-023-096-2

Query Match 85.5%; Score 59; DB 9; Length 694;
Best Local Similarity 83.3%; Pred. No. 0.019;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFQWKRMKVR 12
DB 22 CFQWQNNMKVR 33

RESULT 4
US-09-798-869-6
Sequence 6, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match 73.9%; Score 51; DB 9; Length 15;
Best Local Similarity 75.0%; Pred. No. 0.01;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKRMKVR 12
DB 3 CFQWQNNMKVR 14

RESULT 5
US-09-798-869-3
Sequence 3, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: CAPRINE
US-09-798-869-3

Query Match 71.0%; Score 49; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.022;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 CFQWKRAKRV 11
|:|:|:|:|:
3 CYQWQRRMKL 13

RESULT 6

3-09-798-869-23
Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798.869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 25
TYPE: PPT
ORGANISM: CAPRINE
3-09-798-869-23

Query Match 71.0%; Score 49; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.037;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 CFQWKRAKRV 11
|:|:|:|:|:
3 CYQWQRRMKL 13

RESULT 7

3-09-798-869-7
Sequence 7, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798.869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 15
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
OTHER INFORMATION: sequence)
3-09-798-869-7

Query Match 59.4%; Score 41; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.49;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKRAKRV 11
|:|:|:|:|:
DB 3 CYQWQRRMKL 13

RESULT 8

US-09-798-869-4
Sequence 4, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798.869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 15
TYPE: PPT
ORGANISM: MURINE
US-09-798-869-4

Query Match 58.0%; Score 40; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.71;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKRAKRV 11
|:|:|:|:|:
DB 3 CLRWQNEKRV 13

RESULT 9

US-09-798-869-22
Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798.869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 25
TYPE: PPT
ORGANISM: MURINE
US-09-798-869-22

Query Match 58.0%; Score 40; DB 9; Length 25;
Best Local Similarity 54.5%; Pred. No. 1.2;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKRAKRV 11
|:|:|:|:|:
DB 3 CLRWQNEKRV 13

RESULT 10
US-09-864-761-47985
; Sequence 47985, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-09-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47985
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL096701.14
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EST HUMAN HIT: AW294800.1, EVALUATE 1.00e-06
US-09-864-761-47985

Query Match 55.1%; Score 38; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFQWKR 6
| | | | |
Db 16 CFQWRR 21

RESULT 11
US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8

Query Match 53.6%; Score 37; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 2.3;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKRAMRKV 11
| | | | |
Db 3 CLRQWEMRKV 13

RESULT 12
US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match 53.6%; Score 37; DB 9; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.3;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKRAMRKV 11
| | | | |
Db 3 CFRQWEMKKL 13

RESULT 13
US-09-798-869-30

Sequence 30, Application US/09798869
Publication No. US2003002282A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 15
TYPE: PRT
ORGANISM: BOVINE
-09-798-869-30

Query Match 53.6%; Score 37; DB 9; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.3;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

1 CFQWKRAMRKV 11
|:|:|:|:|:
3 CFQWQRMKKL 13

RESULT 14
-09-888-320-2
Sequence 2, Application US/09888320
Publication No. US20030013090A1
GENERAL INFORMATION:
APPLICANT: Barry III, Clifton E.
APPLICANT: DeBarber, Andrea E.
APPLICANT: Mdululi, Khisimuzi
APPLICANT: Bekker, Linda-Gail
APPLICANT: The Government of the United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REFERENCE: 015280-413100J3
CURRENT APPLICATION NUMBER: US/09/888,320
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 489
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: wild-type Etaa monooxygenase (RV3854C, Eha)

-09-888-320-2
Query Match 53.6%; Score 37; DB 9; Length 489;
Best Local Similarity 54.5%; Pred. No. 66;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 CFQWKRAMRKV 11
|:|:|:|:|:
253 CQKPRRMRKM 263

RESULT 15
-09-738-626-5715
Sequence 5715, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIALI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 5715
LENGTH: 86
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5715

Query Match 52.2%; Score 36; DB 9; Length 86;
Best Local Similarity 45.5%; Pred. No. 18;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 FQWKRAMRKV 12
|:|:|:|:|:
Db 73 FEYRQLRKIR 83

Search completed: February 21, 2003, 08:11:57
Job time : 7.88372 secs

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1 protein - protein search, using sw model

in on: February 21, 2003, 07:48:01 ; Search time 10.6047 Seconds
(without alignments)
108.784 Million cell updates/sec

tle: US-09-743-107b-93

fect score: 69

quence: 1 CFQWKRAVRKVR 12

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 283224 seqs, 96134422 residues

al number of hits satisfying chosen parameters: 283224

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

itabase :

PIR 73:*

1: pirl1:*

2: pirl2:*

3: pirl3:*

4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	59	85.5	711	1	TFHUL
2	49	71.0	708	2	lactoferrin - goat
3	46	66.7	33	2	lactoferrin - sheep
4	45	65.2	275	2	hypothetical prote
5	43	62.3	206	2	pyridoxamine 5'-ph
6	43	62.3	206	2	pyridoxamine 5'-ph
7	43	62.3	208	2	probable pyridoxam
8	42	60.9	1135	2	phytochrome C - so
9	41	59.4	1391	2	hypothetical prote
10	41	59.4	1397	2	protein F09C3.1 [i
11	40	58.0	707	1	lactoferrin precu
12	39	56.5	453	2	hypothetical prote
13	39	56.5	458	2	dyein beta heavy
14	38	55.1	275	2	32x protein - vacc
15	38	55.1	377	2	hypothetical prote
16	38	55.1	377	2	35k myristylprotei
17	38	55.1	377	2	A16L protein - vac
18	38	55.1	378	2	I42518
19	38	55.1	500	2	ADP ATP carrier pr
20	38	55.1	2594	2	kinase-related pro
21	37	53.6	202	2	hypothetical prote
22	37	53.6	380	2	hypothetical prote
23	37	53.6	433	2	hypothetical prote
24	37	53.6	489	2	probable monooxyge
25	37	53.6	530	2	calnexin-like prot
26	37	53.6	532	2	calnexin homolog -
27	37	53.6	584	2	hypothetical prote
28	37	53.6	775	2	probable vacuolar
29	37	53.6	932	2	hypothetical prote

phytochrome - Scot
hypothetical prote
hypothetical prote
F1511.22 (imported
hypothetical prote
gene D5 protein -
33.3K hypothetical regu
transcription regul
gene 20 protein -
hypothetical prote
actin-like protein
calnexin - maize (
cytochrome P450 ho
cytochrome P450 CY
cytochrome P450 (C
cytochrome P450 CP

ALIGNMENTS

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence, revision 21-Nov-1997 #text change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S743

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R:Rey, M.W.; Meloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactoferi

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52659; NID:G263311; PIDN:AAB24677.1; PID:G263312

A:Experimental source: placenta

A:Note: sequence extracted from NCBI backbone (NCBIIP:122202)

R:Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049056

A:Accession: S15853

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: Protein

A:Residues: 20-28, X, 30-31 <ST2>

```

;Rado, T.A.; Wei, X.; Benz Jr., E.J.
;J Biol Chem 270, 389-393, 1997
;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
;Reference number: S07160; MUID:88001031; PMID:3477300
;Accession: S07160
;Molecule type: mRNA
;Residues: 436-487; 'A', 489-711 <RAD>
;Cross-references: EMBL:M8642; NID:G186815; PIDN:AAA86665.1; PID:G386855
;Panella, I.J.; Liu, Y.; Huang, A.T.; Feng, C.T.
;J Biol Chem 270, 3037-3043, 1997
;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
;Reference number: A61169; MUID:91235214; PMID:1674448
;Accession: A61169
;Status: not compared with conceptual translation
;Molecule type: mRNA
;Residues: 3-701; 'SWKPNV' <PAN>
;Experimental source: normal breast tissue
;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, F.; Schoentgen, F.; Legrand, D.; Spik, G.;
;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
;Eur J Biochem 241, 303-308, 1996
;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity chromatography
;Reference number: S74119; MUID:97054624; PMID:8898921
;Accession: S74119
;Molecule type: protein
;Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOV>
;Experimental source: neutrophil granulocytes
;Genetics:
;Gene: GDB:LTF
;Cross-references: GDB:119368; OMIM:150210
;Map position: 3q21-3q23
;Superfamily: transferrin; transferrin repeat homology
;Keywords: duplication; glycoprotein; iron binding; milk
;1-19/Domain: signal sequence #status predicted <SIG>
;120-711/Product: lactoferrin #status experimental <MAT>
;21-356/Domain: transferrin repeat homology <TRH1>
;360-699/Domain: transferrin repeat homology <TRH2>
;29-65;39-56;135-218;177-193;190-201;251-265;503-697;595-609/Disulfide bonds: #status experimental
;157;498/Binding site: carbonyldehydrate (Asn) (covalent) #status experimental
;368-400;378-391;425-706;447-669;479-554;513-527;524-537;647-652/Disulfide bonds: #status experimental

Query Match 85.5%; Score 59; DB 1; Length 711;
Best Local Similarity 83.3%; Pred. No. 0.013;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

y 1 CFQWKRAMRKVR 12
b 39 CFQWKRAMRKVR 50
|||||
|

RESULT 2
;Lactoferrin - goat
;Species: Capra aegagrus hircus (domestic goat)
;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
;Accession: JC2323
;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
;Biochem Biophys Res Commun 203, 1324-1332, 1994
;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
;Reference number: JC2323; MUID:94380047; PMID:8093048
;Accession: JC2323
;Molecule type: mRNA
;Residues: 1-708 <LEP>
;Superfamily: transferrin; transferrin repeat homology
;Keywords: duplication; glycoprotein
;359-686/Domain: transferrin repeat homology <TRH2>
;252;300;387;495;564/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match 71.0%; Score 49; DB 2; Length 708;
Best Local Similarity 63.6%; Pred. No. 0.79;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CFQWKRAMRKVR 11
b 38 CFQWKRAMRKVR 48
|||||
|

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RESULT 3
;Lactoferrin - sheep (fragment)
;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
;Accession: S52107
;Qian, Z.F.; Jolles, P.; Migliore-Samouri, D.; Fiat, A.M.
;Biochim Biophys Acta 1243, 25-32, 1995
;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet aggregation
;Reference number: S52107; MUID:95127729; PMID:7827104
;Accession: S52107
;Status: preliminary
;Molecule type: protein
;Residues: 1-33 <QIA>
;Superfamily: transferrin; transferrin repeat homology
;Keywords: duplication

```

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Query Match 66.7%; Score 46; DB 2; Length 33;
Best Local Similarity 54.5%; Pred. No. 0.15;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

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QY 1 CFQWKRAMRKVR 11
b 19 CFQWKRAMRKVR 29
|||||
|

```

```

RESULT 4
;Hypothetical protein F53H4.4 - Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
;Accession: T22597
;R.Dobson, R.
;Submitted to the EMBL Data Library, October 1996
;Reference number: Z19587
;Accession: T22597
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-275 <WIL>
;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
;Experimental source: clone F53H4
;Genetics:
;Gene: CESP:F53H4.4
;Map position: X
;Introns: 67/1; 153/1
;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4

```

```

Query Match 65.2%; Score 45; DB 2; Length 275;
Best Local Similarity 72.7%; Pred. No. 1.7;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 FQWKRAMRKVR 12
b 262 FQWKRAMRKVR 272
|||||
|

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RESULT 5
;Pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (str. H97451)
;Species: Agrobacterium tumefaciens
;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
;Accession: H97451
;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

```

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* 294, 2323-2328, 2001
 Reference number: A97359; PMID:11743194
 Accession: H97451
 Status: preliminary
 Molecule type: DNA
 Residues: 1-206 <KUR>
 Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:gl15155733; GSPDB:GN00169
 Genes: AGR_C1381
 Map position: circular chromosome
 Superfamily: pyridoxamine-phosphate oxidase

Query Match 62.3%; Score 43; DB 2; Length 206;
 Best Local Similarity 58.3%; Pred. No. 2.9;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 CFQWKRAKRV 12
 |||||
 88 CFHWKSLRRQVR 99
 |||||

RESULT 6
 12670
 pyridoxamine 5'-phosphate oxidase [imported] - *Agrobacterium tumefaciens* (strain C58, Du
 Species: *Agrobacterium tumefaciens*
 Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
 Accession: AB2670
 Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 age, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 Karp, P.; Romero, P.; Zhang, S.
 Title: 294, 2317-2323, 2001
 Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 er, E.W.
 Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 Reference number: AB2577; PMID:11743193
 Accession: AB2670
 Status: preliminary
 Molecule type: DNA
 Residues: 1-206 <KUR>
 Cross-references: GB:AE008688; PIDN:AAI41776.1; PID:gl17739129; GSPDB:GN00186
 Experimental source: strain C58 (Dupont)
 Genes: pdxH
 Map position: circular chromosome
 Superfamily: pyridoxamine-phosphate oxidase

Query Match 62.3%; Score 43; DB 2; Length 206;
 Best Local Similarity 58.3%; Pred. No. 2.9;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 CFQWKRAKRV 12
 |||||
 88 CFHWKSLRRQVR 99
 |||||

RESULT 7
 13441
 cobable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - *Brucella melitensis* (s
 Species: *Brucella melitensis*
 Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
 Accession: AG3441
 DelVecchio, V.G.; Kaparal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
 Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
 oc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 Reference number: AB3252; PMID:11756688
 Accession: AG3441
 Status: preliminary
 Molecule type: DNA
 Residues: 1-208 <KUR>
 Cross-references: GB:AE008917; PIDN:AAI52698.1; PID:gl17983525; GSPDB:GN00190

A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI1517
 A:Map position: 1
 C:Superfamily: pyridoxamine-phosphate oxidase
 C:Keywords: oxidoreductase

Query Match 62.3%; Score 43; DB 2; Length 208;
 Best Local Similarity 58.3%; Pred. No. 2.9;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFQWKRAKRV 12
 |||||
 Db 90 CFHWKSLRRQVR 101
 |||||

RESULT 8
 T14803
 phytochrome C - sorghum
 C:Species: *Sorghum bicolor* (sorghum)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
 C:Accession: T14803
 R.Childe, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet,
 submitted to the EMBL Data Library, April 1996
 A:Reference number: Z18186
 A:Accession: T14803
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-1135 <CHI>
 A:Cross-references: EMBL:U56731; NID:gl800218; PID:gl800219
 C:Genetics:
 A:Gene: PHYC
 C:Superfamily: phytochrome; phytochrome homology
 C:Keywords: chromoprotein; dimer; photoreceptor; phytochromobilin; transcription regulati
 F.65-58/Domain: phytochrome homology <PHY>
 F.321/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 60.9%; Score 42; DB 2; Length 1135;
 Best Local Similarity 45.5%; Pred. No. 22;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKRAKRV 11
 |||||
 Db 775 CLEWKAQKI 785
 |||||

RESULT 9
 T20642
 hypothetical protein F09C3.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T20642
 R.Lennard, N.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: Z19304
 A:Accession: T20642
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1391 <WIL>
 A:Cross-references: EMBL:Z92781; PIDN:CAB07179.2; GSPDB:GN00019; CESP:F09C3.1
 A:Experimental source: clone F09C3
 C:Genetics:
 A:Gene: CESP:F09C3.1
 A:Map position: 1
 A:Introns: 53/2; 134/3; 283/1; 662/1; 731/3; 787/1; 976/3; 1043/2; 1171/3; 1267/2; 1354/3

Query Match 59.4%; Score 41; DB 2; Length 1391;
 Best Local Similarity 70.0%; Pred. No. 40;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWKRAKRV 12
 |||||
 Db 122 QWRRAKRV 131
 |||||

```

hypothetical protein YDR125c - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein YD9727.20C
C/Species: Saccharomyces cerevisiae
C/Date: 19-May-1999 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
R/Murphy, L.; Shore, L.; Harris, D.
R/Accession: S52690
Submitted to the EMBL Data Library, March 1995
A/Reference number: S52671
A/Accession: S52690
A/Molecule type: DNA
A/Residues: 1-453 <MUR>
A/Cross-references: EMBL:Z48758; NID:g747879; PIDN:CAA88678.1; PID:g747899; MIPS:YDR125c
C/Genetics:
A/Genes: SGD:ECM18
A/Cross-references: SGD:S0002532; MIPS:YDR125c
A/Map position: 4R
C/Supfamily: hypothetical protein YDR125c

Query Match 56.5%; Score 39; DB 2; Length 453;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFQWKRAVRKVR 12
Db 24 CYWQKRAVHNSR 35

RESULT 13
T08030
dynein beta heavy chain - Chlamydomonas reinhardtii
C/Species: Chlamydomonas reinhardtii
C/Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
R/Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A/Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A/Reference number: Z16302; MUID:94274778; PMID:8006077
A/Accession: T08030
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-4568 <MIT>
A/Cross-references: EMBL:U02863; NID:g409965; PIDN:AAA19956.1; PID:g514215
A/Experimental source: strain 2igr
C/Genetics:
A/Genes: ODA4
A/Map position: IX
A/Intons: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
3334/3; 3686/3; 3882/3; 4240/3
C/Supfamily: dynein heavy chain, ciliary
C/Keywords: nucleotide binding; P-loop
F/1919-1926/Region: nucleotide-binding motif A (P-loop)
F/2202-2209/Region: nucleotide-binding motif A (P-loop)
F/2530-2537/Region: nucleotide-binding motif A (P-loop)

Query Match 56.5%; Score 39; DB 2; Length 4568;
Best Local Similarity 41.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKRAVRKVR 12
Db 1852 CFQWQSLRYIQ 1863

RESULT 14
A36415
32K protein - vaccinia virus (strain WR) (fragment)
C/Species: vaccinia virus
C/Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000
C/Accession: A36415
R/Pacha, R.F.; Meis, R.J.; Condit, R.C.
J. Virol. 64, 3853-3863, 1990
A/Title: Structure and expression of the vaccinia virus gene which prevents virus-induced
A/Reference number: A36415; MUID:90317884; PMID:2370683

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roten F09C3.1 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
R/Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A/Reference number: A75000; MUID:99069613; PMID:9851916
Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
Accession: E87998
Status: preliminary
Molecule type: DNA
Residues: 1-1397 <STO>
Cross-references: GB:chr_I; PIDN:CAB07179.1; PID:g3875639; GSPDB:GN00019; CESP:F09C3.1
Genetics:
Gene: F09C3.1
Map position: 1

Query Match 59.4%; Score 41; DB 2; Length 1397;
Best Local Similarity 70.0%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Y 3 QWKRAVRKVR 12
b 122 QWRRAVESVR 131

RESULT 11
28438
actoferrin precursor - mouse
N/Alternate names: lactotransferrin
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R/Pentecost, B.T.; Teng, C.T.
Biol. Chem. 262, 10134-10139, 1987
A/Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretory cells
A/Reference number: A92596; MUID:87280033; PMID:3611056
A/Accession: A28438
A/Molecule type: mRNA
A/Residues: 3-707 <PEN>
Cross-references: EMBL:J03298
Liu, Y.; Teng, C.T.
Biol. Chem. 266, 21880-21885, 1991
A/Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A/Reference number: A41205; MUID:92042099; PMID:1939212
A/Accession: A41205
A/Molecule type: DNA
A/Residues: 1-15 <LIU>
Cross-references: GB:M74778
Supfamily: transferrin; transferrin repeat homology
Keywords: duplication; glycoprotein
1-19/Domain: signal sequence #status predicted <SIG>
20-707/Product: lactotransferrin #status predicted <MAT>
358-695/Domain: transferrin repeat homology <RH2>
494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.0%; Score 40; DB 1; Length 707;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Y 1 CFQWKRAVRKVR 11
b 37 CLRQWQNEVRK 47

RESULT 12
152690

```

Accession: A36415
Status: preliminary
Molecule type: DNA
Residues: 1-275 <PAC>
Cross-references: EMBL:M32064; NID:G335834; PIDN:AAA48348.2; PID:G7555635

Query Match 55.1%; Score 38; DB 2; Length 275;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 CFQWKRAMRK 10
| : | | | |
185 CLEWLRKAKK 194

RESULT 15
:8558
pothetical protein Al7L - variola major virus
Species: variola major virus
Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
Accession: T28558
Masung, R.F.; Zeposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
ture 366, 748-751, 1993
Title: Potential virulence determinants in terminal regions of variola smallpox virus
Reference number: Z20488; MUID:94088747; PMID:8264798
Accession: T28558
Status: preliminary; translated from GB/EMBL/DBJ
Molecule type: DNA
Residues: 1-377 <MAS>
Cross-references: EMBL:L22579; NID:G623595; PIDN:AAA60868.1; PID:G439038
Experimental source: strain Bangladesh-1975

Query Match 55.1%; Score 38; DB 2; Length 377;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 CFQWKRAMRK 10
| : | | | |
185 CLEWLRKAKK 194

Search completed: February 21, 2003, 08:02:48
Job time : 12.6047 secs

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protein - protein search, using sw model

on: February 21, 2003, 07:28:06 ; Search time 5.2093 Seconds
(without alignments)
95.544 Million cell updates/sec

file: US-09-743-107B-93
quence score: 69
rfect score: 1
CFQWKEAMKVR 12

ring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 112892 seqs, 41476328 residues

tal number of hits satisfying chosen parameters: 112892

imum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

sult	No.	Score	Query Match	Length	ID	Description
1	59	85.5	711	1	TRFL HUMAN	P02788 homo sapien
2	49	71.0	708	1	TRFL CAMDR	Q9tumo camelus dro
3	49	71.0	708	1	TRFL CAPHI	Q29477 capra hircu
4	42	60.9	1135	1	PHYC SORBI	P93528 sorghum bic
5	40	58.0	1077	1	TRFL MOUSE	P08071 mus musculu
6	40	58.0	1137	1	PHYC ORISA	Q92w19 oryza sativ
7	39	56.5	232	1	NLA DROME	Q9xz18 drosophila
8	39	56.5	4568	1	DYHE CHLRE	Q39565 chlamydomon
9	38	55.1	146	1	RPOB LIBAF	P41187 liberibacte
10	38	55.1	275	1	VAL6 VACCV	P15710 vaccinia vi
11	38	55.1	378	1	VAL6 VACCC	P20993 vaccinia vi
12	38	55.1	500	1	TLCE RICPR	C05962 rickettsia
13	38	55.1	856	1	ENV HV2NZ	P05883 human immun
14	38	55.1	2594	1	7LES DROVI	P20806 drosophila
15	37	53.6	528	1	CAX2 ARATH	Q38798 arabidopsis
16	37	53.6	530	1	CAX1 ARATH	P29402 arabidopsis
17	37	53.6	1131	1	PHY FINSY	Q41046 pinus sylve
18	36	52.2	1133	1	D5 DICDI	P10382 dictyosteli
19	36	52.2	224	1	Y35A MYCGE	Q92b72 mycoplasma
20	36	52.2	303	1	UL24 HSVSA	Q01005 herpesvirus
21	36	52.2	318	1	FX24 HUMAN	Q75426 homo sapien
22	36	52.2	502	1	C932 SOYBN	Q42799 glycine max
23	36	52.2	509	1	C931 SOYBN	Q42798 glycine max
24	36	52.2	510	1	C933 SOYBN	Q81973 glycine max
25	36	52.2	538	1	RO60 HUMAN	P10155 homo sapien
26	36	52.2	538	1	RO60 MOUSE	Q08848 mus musculu
27	36	52.2	538	1	RO60 XENLA	P42700 xenopus lae
28	36	52.2	712	1	ENV HV2S2	P32536 human immun
29	36	52.2	859	1	ENV HV2ST	P20872 human immun
30	36	52.2	1111	1	PHYC ARATH	P14714 arabidopsis
31	36	52.2	1156	1	PHYE SOYBN	P42499 glycine max
32	36	52.2	1164	1	PHYD ARATH	P42497 arabidopsis
33	36	52.2	1172	1	PHYE ARATH	P14713 arabidopsis

34	36	52.2	2554	1	7LES DROME	P13368 drosophila
35	35	50.7	151	1	SYB2 RHIME	Q923q1 rhizobium m
36	35	50.7	264	1	CHHL CANAL	P33700 candida alb
37	35	50.7	351	1	NOV CHICK	P28686 gallus gall
38	35	50.7	485	1	GLGA BACST	O08328 bacillus st
39	35	50.7	558	1	NCAP LYCVA	P09992 lymphocytic
40	35	50.7	558	1	NCAP LYCVW	P07400 lymphocytic
41	35	50.7	857	1	ENV HV2KR	Q74126 human immun
42	35	50.7	1121	1	PHY2 CERPU	O39557 ceratodon p
43	35	50.7	1132	1	PHY1 PHYPA	P36505 physcomitre
44	35	50.7	1179	1	ATX1 ARATH	Q91t02 arabidopsis
45	35	50.7	1214	1	TSGA RAT	Q63679 rattus norv

ALIGNMENTS

RESULT 1
TRFL_HUMAN
ID TRFL_HUMAN STANDARD; PRT; 711 AA.
AC P02788; Q16780; Q16785; Q16789; Q00756; Q9H1Z3; Q96KZ4;
AC Q96KZ5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrroxin A;
DE Lactoferrroxin B; Lactoferrroxin C].
GN LFP OR LF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90384839; PubMed=2402455;
RA Rey M.W., Woloshuk S.I., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RT Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RC Conneely O.N.;
RT Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang Q., Jimenez-Flores R., Richardson T.;
RT "Molecular cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RT "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cheng H., Chen X., Huan L.;
RT "cDNA Cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]

SEQUENCE OF 3-711 FROM N.A.
P TISSUE=Mammary gland;
C MEDLINE=90326549; PubMed=2374734;
A Powell M.J., Ogden J.E., human lactoferrin cDNA.";
I Nucleic Acids Res. 18:4013-4013(1990).
L [9]
P SEQUENCE OF 20-711.
P MEDLINE=85076567; PubMed=6510420;
K Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
A Legrand D., Spik G., Montreuil J., Jolles P.,
I "Human lactotransferrin: amino acid sequence and structural
I comparisons with other transferrins.";
L Eur. J. Biochem. 145:659-666(1984).
L [10]
P PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
P MEDLINE=82046817; PubMed=6794640;
K Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
A Jolles P.;
I "The present state of the human lactotransferrin sequence. Study and
I alignment of the cyanogen bromide fragments and characterization of
I N- and C-terminal domains.";
L Biochim. Biophys. Acta 670:243-254(1981).
L [11]
P SEQUENCE OF 609-711.
P MEDLINE=82262043; PubMed=7049727;
K Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
A Jolles P.;
I "An 88 amino acid long C-terminal sequence of human
I lactotransferrin.";
L FEBS Lett. 142:107-110(1982).
L [12]
P SEQUENCE OF 436-711 FROM N.A.
P MEDLINE=88001031; PubMed=3477300;
X Rado T.A., Wei X., Benz E.J. Jr.;
I "Isolation of lactoferrin cDNA from a human myeloid library and
I expression of mRNA during normal and leukemic myelopoiesis.";
L Blood 70:989-993(1987).
L [13]
P SEQUENCE OF 237-711 FROM N.A.
P McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
A Nham M., Parrell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
A Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
A Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
A Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
A Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
A Segripanti J.L.;
I Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
L [14]
P X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
P MEDLINE=90064528; PubMed=2585506;
X Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
A "Structure of human lactoferrin: crystallographic structure analysis
I and refinement at 2.8-A resolution.";
L J. Mol. Biol. 209:711-734(1989).
L [15]
P X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
P Haridas M., Anderson B.F., Baker E.N.;
A "Structure of human diferric lactoferrin refined at 2.2-A
I resolution.";
L Acta Crystallogr. D 51:629-646(1995).
L [16]
P X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
P MEDLINE=97156796; PubMed=9003186;
X Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
A Baker E.N.;
I "Maturation of the histidine ligand in human lactoferrin: iron
I binding properties and crystal structure of the histidine-
I 253->-methionine mutant.";
L Biochemistry 36:341-346(1997).
L [17]
P X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
P MEDLINE=99190892; PubMed=10089347;
X Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
I "Structure of recombinant human lactoferrin expressed in Aspergillus
I awamori.";
L Acta Crystallogr. D 55:403-407(1999).
L [18]
P X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
P MEDLINE=99192677; PubMed=10089508;
X Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
I "Structure of human apolactoferrin at 2.0-A resolution. Refinement
I and analysis of ligand-induced conformational change.";
L Acta Crystallogr. D 54:1319-1335(1998).
L [19]
P CHARACTERIZATION OF LACTOFERROXINS.
P MEDLINE=91166929; PubMed=1369293;
X Tani F., Iio K., Chiba H., Yoshikawa M.;
I "Isolation and characterization of opioic antagonist peptides derived
I from human lactoferrin.";
L Agric. Biol. Chem. 54:1803-1810(1990).
L [20]
P VARIANTS THR-30 AND ARG-48.
P PubMed=9873089;
X Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
A Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
A Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
A El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
A Hejtmancik J.F., Teng C.T.;
I "Familial subepithelial corneal amyloidosis (gelatinous drop-like
I corneal dystrophy): exclusion of linkage to lactoferrin gene.";
L Mol. Vision 4:31-32(1998).
L [21]
P FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
C CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
C OF AN ANION, USUALLY BICARBONATE.
C [22]
P FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST
C ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
C LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
C FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
C [23]
P SUBUNIT: MONOMER.
C [24]
P SUBCELLULAR LOCATION: Secreted.
C [25]
P DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
C [26]
P SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
C [27]
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C or send an email to license@isb-sib.ch).
C [28]
P EMBL; X53961; CAA37914.1; -
P EMBL; U07643; AAB60324.1; -
P EMBL; M93150; AAA36159.1; -
P EMBL; M83202; AAA59511.1; -
P EMBL; M83205; AAA58656.1; -
P EMBL; M18642; AAA86665.1; -
P EMBL; AF32168; AAG48753.1; -
P EMBL; BC015822; AAH15822.1; -
P EMBL; BC015823; AAH15823.1; -
P EMBL; M73700; AAA59479.1; -
P EMBL; X52941; CAA37116.1; -
P EMBL; U95626; AAB57795.1; -
P PIR; S11228; TFFUL.
P PDB; 1LCF; 31-AUG-94.
P PDB; 1LCT; 31-OCT-93.
P PDB; 1LFG; 31-JUL-94.
P PDB; 1LFH; 31-OCT-93.
P PDB; 1LEI; 31-OCT-93.
P PDB; 1LGB; 31-AUG-94.
P PDB; 1LGC; 31-AUG-94.
P PDB; 1BXA; 08-NOV-96.
P PDB; 1DSN; 08-MAR-96.
P PDB; 1HSE; 12-MAR-97.
P PDB; 1VFD; 21-APR-97.

Query Match 85.5%; Score 59; DB 1; Length 711;
 Best Local Similarity 83.3%; Pred. No. 0.0028;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 CFQWKRMRKVR 12
 |||||:|||||
 39 CFQWQRMRKVR 50

SULT 2

TRFL CAMDR STANDARD; PRT; 708 AA.
 Q9TUM0; Q9WZS5;
 16-OCT-2001 (Rel. 40, Created)
 16-OCT-2001 (Rel. 40, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 Lactotransferrin precursor (lactoferrin).
 LTF.
 Camelus dromedarius (Dromedary) (Arabic camel).
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 NCBI_TaxID=9838;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=Sonali; TISSUE=lactating mammary gland;
 Kappeler S.R.; Ackermann M.; Farah Z.; Fuhan Z.;
 "Sequence analysis of camel (Camelus dromedarius) lactoferrin."
 Int. Dairy J. 9:481-486(1999).
 [2]

SEQUENCE FROM N.A.

TISSUE=Mammary gland;
 Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 -!- SUBUNIT: MONOMER (BY SIMILARITY).
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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 or send an email to license@isb-sib.ch.

EMBL; AJ131674; CAB53387.1; -;
 EMBL; AF165879; AAF82241.1; -;
 HSSP; O77811; 1BIX.
 InterPro; IPR001156; Transferrin.
 Pfam; PF00405; transferrin; 2.
 PRINTS; PR00422; TRANSFERRIN.
 SMART; SM00094; TR_FER; 2.
 PROSITE; PS00205; TRANSFERRIN_1; 2.
 PROSITE; PS00206; TRANSFERRIN_2; 2.
 PROSITE; PS00207; TRANSFERRIN_3; 2.
 Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 Signal.
 SIGNAL
 CHAIN 1 19 BY SIMILARITY.
 REPEAT 20 708 LACTOTRANSFERRIN.
 REPEAT 20 363 1.
 REPEAT 364 708 2.
 DISULFID 28 64 BY SIMILARITY.
 DISULFID 38 55 BY SIMILARITY.
 DISULFID 134 217 BY SIMILARITY.
 DISULFID 176 192 BY SIMILARITY.
 DISULFID 189 200 BY SIMILARITY.
 DISULFID 250 264 BY SIMILARITY.
 DISULFID 367 399 BY SIMILARITY.

DISULFID 377 390 BY SIMILARITY.
 DISULFID 424 703 BY SIMILARITY.
 DISULFID 444 666 BY SIMILARITY.
 DISULFID 476 551 BY SIMILARITY.
 DISULFID 500 694 BY SIMILARITY.
 DISULFID 510 524 BY SIMILARITY.
 DISULFID 521 534 BY SIMILARITY.
 DISULFID 592 606 BY SIMILARITY.
 DISULFID 644 649 BY SIMILARITY.
 METAL 79 79 IRON 1 (BY SIMILARITY).
 METAL 111 111 IRON 1 (BY SIMILARITY).
 METAL 211 211 IRON 1 (BY SIMILARITY).
 METAL 272 272 IRON 1 (BY SIMILARITY).
 METAL 414 414 IRON 2 (BY SIMILARITY).
 METAL 452 452 IRON 2 (BY SIMILARITY).
 METAL 545 545 IRON 2 (BY SIMILARITY).
 METAL 614 614 IRON 2 (BY SIMILARITY).
 BINDING 140 140 ANION (BY SIMILARITY).
 BINDING 482 482 ANION (BY SIMILARITY).
 CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 385 385 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 537 537 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 594 594 N-LINKED (GLCNAC. .) (POTENTIAL).
 CONFLICT 261 261 F -> S (IN REF. 2).
 CONFLICT 304 304 G -> A (IN REF. 2).
 CONFLICT 330 330 S -> P (IN REF. 2).
 CONFLICT 492 494 LLS -> PLF (IN REF. 2).
 CONFLICT 506 506 L -> F (IN REF. 2).
 CONFLICT 609 609 A -> P (IN REF. 2).
 CONFLICT 642 642 R -> Q (IN REF. 2).
 SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 71.0%; Score 49; DB 1; Length 708;

Best Local Similarity 66.7%; Pred. No. 0.19;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKRMRKVR 12
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 DB 38 CAQWQRMRKVR 49

RESULT 3

TRFL CAPHI STANDARD; PRT; 708 AA.
 ID TRFL CAPHI STANDARD; PRT; 708 AA.
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OC NCBI_TaxID=9925;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=94380047; PubMed=8093048;
 RA le Provost F., Nocard M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 relevant locus to bovine U12 syntenic group."
 RL Biochem Biophys Res Commun. 203:1324-1332(1994).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.

C -I- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 C -I- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 C
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 C or send an email to license@isb-sib.ch).
 C
 C EMBL; U53857; AAA97958.1; --
 C EMBL; X78902; CAA55517.1; --
 C HSP; O77698; 1CE2.
 C InterPro; IPR001156; Transferrin.
 C Pfam; PF00405; transferrin; 2.
 C PRINTS; PR00422; TRANSFERRIN.
 C SMART; SM00094; TF_FER; 2.
 C PROSITE; PS00205; TRANSFERRIN 1; 2.
 C PROSITE; PS00206; TRANSFERRIN 2; 2.
 C PROSITE; PS00207; TRANSFERRIN 3; 2.
 C Transports; Iron transport; Glycoprotein; Metal-binding; Repeat;
 C Signal.
 C
 C 1 19 BY SIMILARITY
 C CHAIN 20 708 LACTOTRANSFERRIN.
 C REPEAT 20 363 1.
 C REPEAT 364 708 2.
 C DISULFID 28 64 BY SIMILARITY.
 C DISULFID 38 55 BY SIMILARITY.
 C DISULFID 134 217 BY SIMILARITY.
 C DISULFID 176 192 BY SIMILARITY.
 C DISULFID 189 200 BY SIMILARITY.
 C DISULFID 250 264 BY SIMILARITY.
 C DISULFID 367 399 BY SIMILARITY.
 C DISULFID 377 390 BY SIMILARITY.
 C DISULFID 424 703 BY SIMILARITY.
 C DISULFID 444 666 BY SIMILARITY.
 C DISULFID 476 551 BY SIMILARITY.
 C DISULFID 500 694 BY SIMILARITY.
 C DISULFID 510 524 BY SIMILARITY.
 C DISULFID 521 534 BY SIMILARITY.
 C DISULFID 592 606 BY SIMILARITY.
 C DISULFID 644 649 BY SIMILARITY.
 C METAL 79 79 IRON 1 (BY SIMILARITY).
 C METAL 111 111 IRON 1 (BY SIMILARITY).
 C METAL 211 211 IRON 1 (BY SIMILARITY).
 C METAL 272 272 IRON 1 (BY SIMILARITY).
 C METAL 414 414 IRON 2 (BY SIMILARITY).
 C METAL 452 452 IRON 2 (BY SIMILARITY).
 C METAL 545 545 IRON 2 (BY SIMILARITY).
 C METAL 614 614 ANION (BY SIMILARITY).
 C BINDING 140 140 ANION (BY SIMILARITY).
 C BINDING 482 482 ANION (BY SIMILARITY).
 C CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
 C CONFLICT 56 56 I -> V (IN REF. 2).
 C CONFLICT 88 88 L -> R (IN REF. 2).
 C CONFLICT 124 124 Q -> K (IN REF. 2).
 C CONFLICT 154 154 P -> P (IN REF. 2).
 C CONFLICT 304 304 S -> R (IN REF. 2).
 C CONFLICT 414 414 D -> G (IN REF. 2).
 C SEQUENCE 708 AA; 77358 MW; F2EDA3C83539960D CRC64;

Query Match 71.0%; Score 49; DB 1; Length 708;
 Best Local Similarity 63.6%; Pred. No. 0.19;
 Matches 7; Conservative 3; Mismatches 0; Gaps 0;

Y 1 CFQWKRAMRKV 11
 b 38 CYQWRRMKL 48

RESULT 4
 PHYC_SORBI STANDARD; PRT; 1135 AA.
 ID PHYC_SORBI
 AC P93528;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phytochrome C.
 GN PHYC.
 OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Clade;
 OC Panicoideae; Andropogoneae; Sorghum.
 OX NCBI_TaxID=4558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97198556; PubMed=9046599;
 RA Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
 RA Morgan P.W., Mullet J.E.;
 RT "The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
 RT phytochrome B.";
 RL Plant Physiol. 113:611-619(1997).
 CC -I- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
 CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
 CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
 CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCOVERSION OF PFR IN
 CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
 CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
 CC RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
 CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
 CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
 CC PROCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE
 CC EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY
 CC SIMILARITY).
 CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -I- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
 CC -I- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
 CC -I- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
 CC -I- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
 CC -I- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
 CC
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 CC
 CC EMBL; U56731; AAB41399.1; --
 CC InterPro; IPR003594; ATPbind_ATPase.
 CC InterPro; IPR003018; GAF.
 CC InterPro; IPR004359; HIS_KIN_sig.
 CC InterPro; IPR003661; His_kinA.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS_domain.
 CC InterPro; IPR001294; Phytochrome.
 CC Pfam; PF00360; phytochrome; 1.
 CC Pfam; PF00512; signal; 1.
 CC Pfam; PF00389; PAS; 2.
 CC Pfam; PF01590; GAF; 1.
 CC Pfam; PF02518; HATPase_c; 1.
 CC PRINTS; PR01033; PHYTOCHROME.
 CC SMART; SM00065; GAF; 1.
 CC SMART; SM00387; HATPase_c; 1.
 CC SMART; SM00388; HisK_A; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 2.
 CC TIGRFAMs; TIGR00223; sensory_box; 2.
 CC PROSITE; PS0109; HIS_KIN; 1.
 CC PROSITE; PS0112; PAS; 2.

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PROSITE; PS00245; PHYTOCHROME_1; FALSE NEG.
PROSITE; PS00046; PHYTOCHROME_2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
Repeat; Multigene family.
DOMAIN 618 688 PAS 1.
DOMAIN 748 822 PAS 2.
DOMAIN 902 1122 HISTIDINE KINASE.
BINDING 321 321 CHROMOPHORE (BY SIMILARITY).
SEQUENCE 1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;

Query Match 60.9%; Score 42; DB 1; Length 1135;
Best Local Similarity 45.5%; Pred. No. 6.2;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

1 CFQWKRAMRKV 11
| : : : :
775 CLEWKAQKI 785

SULT 5
FL_MOUSE STANDARD; PRT; 707 AA.
P08071; P70690; Q61799; Q922B2;
01-AUG-1998 (Rel. 08, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactoferrin precursor (Lactoferrin).
LTF.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TISSUE=Uterus;
MEDLINE=87280033; PubMed=3611056;
Pentecost B.T.; Teng C.T.;
"Lactoferrin is the major estrogen inducible protein of mouse
uterine secretions.";
J. Biol. Chem. 262:10134-10139(1987).
[2]
SEQUENCE FROM N.A.
TISSUE=Uterus;
Morihashi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
Straussberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE OF 1-14 FROM N.A.
MEDLINE=92042099; PubMed=1939212;
Liu Y.; Teng C.T.;
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885(1991).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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EMBL; J03298; AAA40525.1; -.
EMBL; D88510; BAA13633.1; -.

DR EMBL; BC006904; AAA06904.1; -.
DR EMBL; M74778; AAA39427.1; -.
DR PIR; A28438; A28438.
DR HSP; P02788; 1CB6.
DR MGD; MGI:96837; Ltf.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SMO0094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal.
FT CHAIN 1 19 BY SIMILARITY.
FT REPEAT 20 707 LACTOTRANSFERRIN.
FT REPEAT 20 357 1.
FT REPEAT 358 707 2.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.
FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 263 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 702 720 BY SIMILARITY.
FT DISULFID 423 433 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 IRON 1 (BY SIMILARITY).
FT METAL 110 IRON 1 (BY SIMILARITY).
FT METAL 210 IRON 1 (BY SIMILARITY).
FT METAL 271 IRON 1 (BY SIMILARITY).
FT METAL 413 IRON 2 (BY SIMILARITY).
FT METAL 451 IRON 2 (BY SIMILARITY).
FT METAL 544 IRON 2 (BY SIMILARITY).
FT METAL 613 IRON 2 (BY SIMILARITY).
FT BINDING 139 ANION (POTENTIAL).
FT BINDING 481 ANION (POTENTIAL).
FT CARBOHYD 118 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 494 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).
FT CONFLICT 25 25 R -> Q (IN REF. 2).
FT CONFLICT 82 82 M -> L (IN REF. 2).
FT CONFLICT 359 359 S -> T (IN REF. 2).
FT CONFLICT 382 382 A -> D (IN REF. 1).
FT CONFLICT 449 449 E -> G (IN REF. 2).
FT CONFLICT 629 629 L -> V (IN REF. 1).
SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;

Query Match 58.0%; Score 40; DB 1; Length 707;
Best Local Similarity 54.5%; Pred. No. 8.8;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFQWKRAMRKV 11
| : : : :
Db 37 CLRQWNEMRKV 47

RESULT 6
PHYC ORYSA
ID PHYC ORYSA STANDARD; PRT; 1137 AA.
AC Q9ZW19; P93429;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome C.
GN PHYC.
```

S Oryza sativa (Rice).
 T Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 P Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 K Ehrhartoideae; Oryzaceae; Oryza.
 X NCBI_TaxID=4530;
 [1]
 P SEQUENCE FROM N.A.
 C STRAIN=cv. Nipponbare;
 A Tahir M., Kanegae H., Takano M.;
 I "Phytochrome C (PHYC) gene in rice: isolation and characterization of
 L a complete coding sequence";
 L (in) Plant Gene Register PGR98-210.
 N [2]
 P SEQUENCE OF 275-378 FROM N.A.
 X MEDLINE=97019052; PubMed=8965668;
 K Matthews S., Sharrock R.A.;
 I "The phytochrome gene family in grasses (Poaceae): a phylogeny and
 L evidence that grasses have a subset of the loci found in dicot
 L angiosperms";
 L Mol. Biol. Evol. 13:1141-1150(1996).
 L -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
 L ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
 L MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
 L ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PFR IN
 L PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
 L RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
 L RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
 L GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
 L BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
 L PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS
 L THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
 L -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 L -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
 L -!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
 L -!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
 L -!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
 L -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
 L -----
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 L or send an email to license@isb-sib.ch).
 L -----
 R EMBL; AB018442; BAA74448.1; -;
 R EMBL; U61207; AAB41996.1; -;
 R InterPro: IPR003594; ATPbind_ATPase.
 R InterPro: IPR003018; GAF.
 R InterPro: IPR004359; HIS_KIN_sig.
 R InterPro: IPR003661; His_kinA.
 R InterPro: IPR001610; PAC.
 R InterPro: IPR001294; Phytochrome.
 R Pfam; PF00360; phytochrome.1.
 R Pfam; PF00512; signal.1.
 R Pfam; PF00389; PAS.2.
 R Pfam; PF00390; GAF.1.
 R Pfam; PF02518; HATPase_c.1.
 R PRINTS; PF01033; PHYTOCHROME.
 R SMART; SM00065; GAF.1.
 R SMART; SM00387; HATPase_c.1.
 R SMART; SM00388; HisK_A.1.
 R SMART; SM00086; PAC.1.
 R SMART; SM00091; PAS.2.
 R TIGRfam; TIGR00229; sensory_box.2.
 R PROSITE; PS50109; HIS_KIN.1.
 R PROSITE; PS50112; PAS.2.
 R PROSITE; PS00245; PHYTOCHROME_1; 1.
 R PROSITE; PS00046; PHYTOCHROME_2; 1.
 W Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
 W Repeat; Multigene family.

FT DOMAIN 620 690 PAS 1.
 FT DOMAIN 750 824 PAS 2.
 FT BINDING 904 1124 HISTIDINE KINASE
 FT BINDING 322 322 CHROMOPHORE (BY SIMILARITY).
 FT CONFLICT 279 279 F -> S (IN REF. 2).
 FT CONFLICT 292 292 C -> S (IN REF. 2).
 SQ SEQUENCE 1137 AA; 125982 MW; F2A520181CFE7B32 CRC64;
 Query Match 58.0%; Score 40; DB 1; Length 1137;
 Best Local Similarity 45.5%; Pred. No. 15;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFQKRAMRVK 11
 DB 777 CLEWNEAWQKI 787
 RESULT 7
 NLA_DROME
 ID NLA_DROME STANDARD; PRT; 292 AA.
 AC Q9XZL8; Q9V391;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Nebula protein.
 GN NLA OR CG6072.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McCormick A.V., Goldberg M.L.;
 RT "Gene required for elongation of meiosis I spindle in Drosophila
 RT females.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter B.C., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Franckoch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Casley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Fabros B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders M.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Turner C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*."
 Science 287:2185-2195(2000).
 -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
 -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.

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 EMBL; AF147700; AAF33987.1; -.
 EMBL; AF003712; AAF5285.1; -.
 FlyBase; FBgn0026629; nla.
 SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

 Query Match 56.5%; Score 39; DB 1; Length 292;
 Best Local Similarity 54.5%; Pred.No. 5.3; Mismatches 2; Indels 0; Gaps 0;
 Matches 6; Conservative 3;

 2 FQWKRMRKVR 12
 ||| | : : :
 150 FQWLSRFLRL 160

 SULT 8
 HB CHLRE
 DYHE CHLRE STANDARD; PRT; 4568 AA.
 Q39565;
 01-NOV-1997 (Rel. 35, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 30-MAY-2000 (Rel. 39, Last annotation update)
 Dynein beta chain, flagellar outer arm.
 ODA4 OR ODA-4 OR SUP1.
 Chlamydomonas reinhardtii.
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadaceae; Chlamydomonas.
 NCBI_TaxID=3055;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=21gr;
 MEDLINE=94274778; PubMed=8006077;
 Mitchell D.R., Brown K.S.;
 "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes".
 J. Cell Sci. 107:635-644(1994).
 -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES. DYNEIN HAS ATPASE ACTIVITY.
 -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
 -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.

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 EMBL; U02963; AAA1956.1; -.
 InterPro; IPR004273; Dynein heavy.
 Pfam; PF03028; Dynein heavy; 1.
 Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
 Coiled coil. 277 293 COILED COIL (POTENTIAL).
 DOMAIN

FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
 FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
 FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
 FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
 FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
 FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
 FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
 FT DOMAIN 3339 3425 COILED COIL (POTENTIAL).
 FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
 FT NP_BIND 1919 1926 ATP (POTENTIAL).
 FT NP_BIND 2202 2209 ATP (POTENTIAL).
 FT NP_BIND 2530 2537 ATP (POTENTIAL).
 FT NP_BIND 2879 2886 ATP (POTENTIAL).
 SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

 Query Match 56.5%; Score 39; DB 1; Length 4568;
 Best Local Similarity 41.7%; Pred.No. 96;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

 Qy 1 CFQWKRMRKVR 12
 ||| | : : :
 Db 1852 CFQWQSQLRYIQ 1863

 RESULT 9
 RPOB LIBAF
 ID RPOB LIBAF STANDARD; PRT; 146 AA.
 AC P41187;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
 GN RPOB.
 OS Liberibacter africanus (Liberibacter africanum).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Candidatus Liberibacter.
 OX NCBI_TaxID=34020;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nelspruit;
 RA Planet P., Jagoueix S., Bove J.M., Garnier M.;
 RT "Detection and characterization of the African Citrus Greening Liberibacter by amplification, cloning and sequencing of the rplKALJL-rpoBC operon".
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).
 CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA' CHAIN.
 CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.

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 EMBL; U09675; AAA19557.1; -.
 InterPro; IPR001572; RNA_pol_B.
 Pfam; PF00562; RNA_pol_B; 1.
 DR PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
 KW Transferase; Transcription; DNA-directed RNA polymerase.
 FT NON_TER 146 146
 SQ SEQUENCE 146 AA; 16731 MW; 815D6EDD66F8943 CRC64;

 Query Match 55.1%; Score 38; DB 1; Length 146;

Best Local Similarity 60.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Y 1 CFQWKRMRK 10
| | | | |
b 10 CVQWSRGARK 19

RESULT 10
AL6_VACCC STANDARD; PRT; 275 AA.
C P16710;
T 01-AUG-1990 (Rel. 15, Created)
T 01-AUG-1990 (Rel. 15, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
T Protein A16 (Fragment).
X A16L.
S Vaccinia virus (strain WR).
C Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
C Orthopoxvirus.
X NCBI_TaxID=10254;
K [1]
P SEQUENCE FROM N.A.
K MEDLINE=90317884; PubMed=2370693;
A Facha R.F., Meis R.J., Condit R.C.;
T "Structure and expression of the vaccinia virus gene which prevents
T virus-induced breakdown of RNA.";
J. Virol. 64:3853-3863(1990).
L -1- SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY.

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EMBL; M32084; AAA48348.2; -
PIR; A36415; A36415.
R InterPro; IPR004251; DUF230.
R Pfam; PF03003; DUF230; 1.
T NON TER 275 275
Q SEQUENCE 275 AA; 31811 MW; E2461AB1DB7B93A3 CRC64;
Query Match 55.1%; Score 38; DB 1; Length 275;
Best Local Similarity 60.0%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Y 1 CFQWKRMRK 10
| | | | |
b 185 CLEWLAKRK 194

RESULT 11
AL6_VACCC STANDARD; PRT; 378 AA.
C P20953;
T 01-FEB-1991 (Rel. 17, Created)
T 01-FEB-1991 (Rel. 17, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
T Protein A16.
X A16L.
S Vaccinia virus (strain Copenhagen).
C Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
C Orthopoxvirus.
X NCBI_TaxID=10249;
K [1]
P SEQUENCE FROM N.A.
K MEDLINE=91021027; PubMed=2219722;
A Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
A Paoletti E.;
T "The complete DNA sequence of vaccinia virus.";

RL Virology 179:247-266(1990).
RN [2]
RP COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";
RL Virology 179:517-563(1990).
CC -1- SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY.

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EMBL; M35027; AAA48138.1; -
PIR; I42518; I42518.
R InterPro; IPR004251; DUF230.
R Pfam; PF03003; DUF230; 1.
S SEQUENCE 378 AA; 43561 MW; 05ED614AA1D11A19 CRC64;
Query Match 55.1%; Score 38; DB 1; Length 378;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKRMRK 10
| | | | |
Db 185 CLEWLAKRK 194

RESULT 12
TLCE RICPR STANDARD; PRT; 500 AA.
ID TLCE RICPR
AC O05962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein 5 (ADP/ATP translocase 5).
GN TLCE OR TLC5 OR RP739.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
RN [2]
RP SEQUENCE OF 325-500 FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=97419517; PubMed=9274032;
RA Andersson J.O., Andersson S.G.E.;
RT "Genomic rearrangements during evolution of the obligate
RT intracellular parasite Rickettsia prowazekii as inferred from an
RT analysis of 52015 bp nucleotide sequence.";
RL Microbiology 143:2783-2795(1997).
CC -1- FUNCTION: PROVIDES THE RICKETTSIAL CELL WITH HOST ATP IN
CC EXCHANGE FOR RICKETTSIAL ADP. THIS IS AN OBLIGATE EXCHANGE SYSTEM.
CC THIS ENERGY ACQUIRING ACTIVITY IS AN IMPORTANT COMPONENT OF
CC RICKETTSIAL PARASITISM (BY SIMILARITY)
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE ADP/ATP TRANSLOCASE TLC FAMILY.

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EMBL; AJ235273; CAA15167.1; -
EMBL; Y11778; CAA72457.1; -
InterPro; IPR004667; ADP_ATP_car.
Pfam; PF03219; TFC; 1.
TIGRFAMs; TIGR00769; AAA; 1.
Transmembrane; Transport; ATP-binding; Multigene family;
Complete proteome.
TRANSMEM 26 46 POTENTIAL.
TRANSMEM 62 82 POTENTIAL.
TRANSMEM 94 114 POTENTIAL.
TRANSMEM 149 169 POTENTIAL.
TRANSMEM 184 204 POTENTIAL.
TRANSMEM 224 244 POTENTIAL.
TRANSMEM 287 307 POTENTIAL.
TRANSMEM 328 348 POTENTIAL.
TRANSMEM 357 377 POTENTIAL.
TRANSMEM 381 401 POTENTIAL.
TRANSMEM 469 489 POTENTIAL.
SEQUENCE 500 AA; 57073 MW; FE3DB48D08CF5F72 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 500;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 CFQWGRMKRV 11
||| |||:
482 CFATYIAVRKI 492

SULT 13

V_HV2NZ

ENV HV2NZ STANDARD; PRT; 856 AA.
P05883;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
Human immunodeficiency virus type 2 (isolate NIH-Z) (HIV-2).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11719;
[1]
SEQUENCE FROM N.A.
MEDLINE=8830359; PubMed=3261862;
Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starcich B.R., Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laure F., Arya S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.;
"Genetic variability between isolates of human immunodeficiency virus (HIV) type 2 is comparable to the variability among HIV type 1.";
Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).

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EMBL; J03654; AAB00761.1; -
HIV; J03654; ENV2NIH2.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;

KW Signal. 1 20
FT SIGNAL 21 492
FT CHAIN 493 856
FT CARBOHYD 37 70
FT CARBOHYD 70 70
FT CARBOHYD 79 79
FT CARBOHYD 112 112
FT CARBOHYD 116 116
FT CARBOHYD 128 128
FT CARBOHYD 133 133
FT CARBOHYD 142 142
FT CARBOHYD 182 182
FT CARBOHYD 183 183
FT CARBOHYD 196 196
FT CARBOHYD 228 228
FT CARBOHYD 231 231
FT CARBOHYD 238 238
FT CARBOHYD 262 262
FT CARBOHYD 268 268
FT CARBOHYD 279 279
FT CARBOHYD 290 290
FT CARBOHYD 300 300
FT CARBOHYD 355 355
FT CARBOHYD 390 390
FT CARBOHYD 400 400
FT CARBOHYD 440 440
FT CARBOHYD 457 457
FT CARBOHYD 602 602
FT CARBOHYD 611 611
FT CARBOHYD 627 627
SQ SEQUENCE 856 AA; 99665 MW; A93B0A7E2B881D6 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 856;

Best Local Similarity 60.0%; Pred. No. 25;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 3 QWGRMKRV 12
||| |||:
Db 334 QWKEAMQEVK 343

RESULT 14

7LES_DROVI STANDARD; PRT; 2594 AA.
ID 7LES_DROVI AC P20806;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sevenless protein (EC 2.7.1.112).
GN SEV.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319110; PubMed=2115169;
RA Michael W.M., Bowtell D.D.L., Rubin G.M.;
RT "Comparison of the sevenless genes of Drosophila virilis and Drosophila melanogaster.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5351-5353(1990).
CC -1- FUNCTION: RECEPTOR FOR AN EXTRACELLULAR SIGNAL REQUIRED TO INSTRUCT A CELL TO DIFFERENTIATE INTO A R7 PHOTORECEPTOR. THE LIGAND FOR SEV IS THE BOSS (BRIDE OF SEVENLESS) PROTEIN.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- CAUTION: UNCLEAR WHETHER THE POTENTIAL MEMBRANE SPANNING REGION NEAR THE N-TERMINUS IS PRESENT AS A TRANSMEMBRANE DOMAIN IN THE

 NATIVE PROTEIN OR SERVES AS A CLEAVED SIGNAL SEQUENCE.

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EMBL; M34545; AAA28883.1; -
 ENEM; M34544; AAA28883.1; JOINED.
 ENEM; M34543; AAA28883.1; JOINED.

PIR; A35774; A35774.

HSP; P11362; LFCK.

FlyBase; FBgn013140; Dvir\sev.

InterPro; IPR000719; Euk_pkinase.

InterPro; IPR003961; FN_III.

InterPro; IPR000033; ldl_receptor_rep.

InterPro; IPR002011; RTKkinaseII.

InterPro; IPR001245; Tyr_pkinase.

Pfam; PF00041; fn3; 6.

Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SMC0060; FN3; 5.

SMART; SMC0135; LY; 1.

SMART; SMC0219; TyrcK; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00239; RECEPTOR TYR KIN II; 1.

PROSITE; PS00311; PROTEIN KINASE DOM; 1.

Transferase; Tyrosine-protein kinase; Receptor; Vision; Transmembrane;

Glycoprotein; ATP-binding; Phosphorylation; Repeat.

DOMAIN 1 2139 EXTRACELLULAR (POTENTIAL).

TRANSMEM 2140 2163 CYTOPLASMIC (POTENTIAL).

DOMAIN 2164 2594 POLY-GLN

DOMAIN 356 459 FIBRONECTIN TYPE-III 1.

DOMAIN 464 555 FIBRONECTIN TYPE-III 2.

DOMAIN 835 935 FIBRONECTIN TYPE-III 3.

DOMAIN 1328 1421 FIBRONECTIN TYPE-III 4.

DOMAIN 1706 1816 FIBRONECTIN TYPE-III 5.

DOMAIN 1817 1916 FIBRONECTIN TYPE-III 6.

DOMAIN 1917 2007 FIBRONECTIN TYPE-III 7.

DOMAIN 2057 2063 POLY-ARG.

DOMAIN 2224 2495 PROTEIN KINASE.

NP BIND 2230 2238 ATP (BY SIMILARITY).

BINDING 2257 2257 ATP (BY SIMILARITY).

MOD RES 2391 2391 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 508 508 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 532 532 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 641 641 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 667 667 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 778 778 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 797 797 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 874 874 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 980 980 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1257 1257 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1344 1344 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1382 1382 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1577 1577 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1587 1587 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1665 1665 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1752 1752 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1776 1776 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1824 1824 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1908 1908 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 1966 1966 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 2088 2088 N-LINKED (GLCNAC. .) (POTENTIAL).

SEQUENCE 2594 AA; 289130 MW; 77D8A356CBAD0BBD CRC64;

Query Match 55.1%; Score 38; DB 1; Length 2594;

Best Local Similarity 45.5%; Pred. No. 81;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 CFQWKKAMKRV 11

Db 305 CAQWYRALKKEI 315

RESULT 15

CAX2_ARATH STANDARD; PRT; 528 AA.

ID CAX2_ARATH

AC Q38798;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calnexin homolog 2 precursor.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RA Boyce J.; Coates D.; Evans D.;

RT "Genomic sequence of a calnexin homologue from Arabidopsis thaliana."

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.

CC -! FUNCTION: CALCIUM-BINDING PROTEIN THAT INTERACTS WITH NEWLY SYNTHESIZED GLYCOPROTEINS IN THE ENDOPLASMIC RETICULUM. IT MAY ACT IN ASSISTING PROTEIN ASSEMBLY AND/OR IN THE RETENTION WITHIN THE ER OF UNASSEMBLED PROTEIN SUBUNITS. IT SEEMS TO PLAY A MAJOR ROLE IN THE QUALITY CONTROL APPARATUS OF THE ER BY THE RETENTION OF INCORRECTLY FOLDED PROTEINS (BY SIMILARITY).

CC -! SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic reticulum (By similarity).

CC -! SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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CC ENEM; U08315; AA117742.1; -

DR InterPro; IPR001580; Calreticulin.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR ProDom; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN_1; 1.

DR PROSITE; PS00804; CALRETICULIN_2; 1.

DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.

KW Calcium-binding; Endoplasmic reticulum; Transmembrane; Signal;

Repeat; Chaperone.

FT SIGNAL 1 25 POTENTIAL.

FT CHAIN 26 528 CALNEXIN HOMOLOG 2.

FT DOMAIN 26 466 LUMENAL (POTENTIAL).

FT TRANSMEM 467 487 POTENTIAL.

FT DOMAIN 488 528 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 227 293 4 X APPROXIMATE REPEATS.

FT REPEAT 227 238 1-1.

FT REPEAT 244 255 1-2.

FT REPEAT 263 274 1-3.

FT REPEAT 282 293 1-4.

FT DOMAIN 297 354 4 X APPROXIMATE REPEATS.

FT REPEAT 297 307 2-1.

FT REPEAT 316 326 2-2.

FT REPEAT 330 340 2-3.

FT REPEAT 344 354 2-4.

FT REPEAT 464 464 N-LINKED (GLCNAC. .) (POTENTIAL).

SEQUENCE 528 AA; 60017 MW; C888DA1391B651EE CRC64;
Query Match 53.6%; Score 37; DB 1; Length 528;
Best Local Similarity 50.0%; Pred No. 23;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
1 CFQWKRAMRK 10
|:|:|:|:
315 CGEWRKPMKR 324

arch completed: February 21, 2003, 07:51:40
b time : 6.2093 secs

GenCore version 5.1.3
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protein - protein search, using sw model

on: February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
(without alignments)
114.078 Million cell updates/sec

file: US-09-743-107B-93

fect score: 69

quence: 1 CFQWQRMRKV 12

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 671580 seqs, 206047115 residues

tal number of hits satisfying chosen parameters: 671580

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

tabase :

SPREMBL 21:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mnc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriapi:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB ID	Description
1	54	78.3	711	4 Q8TCD2	Q8tcd2 homo sapien
2	50	72.5	38	4 Q9UCY5	Q9ucy5 homo sapien
3	46	66.7	33	6 Q9TR80	Q9tr80 ovis aries
4	45	65.2	275	5 Q93780	Q93780 caenorhabdi
5	43	62.3	205	16 Q986A0	Q986A0 rhizobium
6	43	62.3	206	16 Q8UHC2	Q8unc2 agrobacteri
7	43	62.3	206	16 Q9ZRH8	Q9zrh8 rhizobium m
8	43	62.3	208	16 Q9YFK3	Q9yfk3 brucella me
9	42	60.9	1121	10 Q9SWS6	Q9sws6 lycopersico
10	41	59.4	508	15 Q74118	Q74118 human immun
11	41	59.4	1391	5 O17772	O17772 caenorhabdi
12	40	58.0	105	10 Q9XFD5	Q9xfds oryza sativ
13	40	58.0	126	15 Q90827	Q90827 human immun
14	40	58.0	148	10 Q9XHP1	Q9xhpi sesamum ind
15	40	58.0	274	4 Q96W21	Q96w21 homo sapien
16	40	58.0	830	10 Q945T7	Q945t7 hordeum vul

17	40	58.0	1137	10 Q9M7A9	Q9m7a9 oryza sativ
18	40	58.0	1139	10 Q8VWN1	Q8vwn1 triticum ae
19	39	56.5	57	4 Q96136	Q96136 homo sapien
20	39	56.5	99	15 P88213	P88213 human immun
21	39	56.5	154	15 Q9E8H5	Q9e8h5 human immun
22	39	56.5	253	12 Q68541	Q68541 horseradish
23	39	56.5	279	16 Q8XSE2	Q8xse2 ralstonia s
24	39	56.5	397	5 Q9U054	Q9u054 giardia lam
25	39	56.5	453	3 Q04623	Q04623 saccharomyc
26	39	56.5	845	15 Q8UNF5	Q8unf5 human immun
27	38	55.1	77	15 Q91683	Q91683 human immun
28	38	55.1	80	15 Q91699	Q91699 human immun
29	38	55.1	91	15 Q77855	Q77855 human immun
30	38	55.1	117	15 Q73233	Q73233 human immun
31	38	55.1	133	15 Q90822	Q90822 human immun
32	38	55.1	207	10 Q9SML1	Q9sml1 ciccer ariet
33	38	55.1	240	10 Q9SML2	Q9sml2 ciccer ariet
34	38	55.1	306	4 Q8TAX2	Q8tax2 homo sapien
35	38	55.1	377	12 Q99164	Q99164 variola vir
36	38	55.1	377	12 Q85389	Q85389 variola maj
37	38	55.1	377	12 Q33122	Q33122 vaccinia vi
38	38	55.1	377	12 Q8V2N9	Q8v2n9 camelpox vi
39	38	55.1	377	12 Q8QMT7	Q8qmt7 cowpox viru
40	38	55.1	466	4 Q9NUS2	Q9nus2 homo sapien
41	38	55.1	499	10 Q9XFX1	Q9xfx1 ciccer ariet
42	38	55.1	659	15 Q8DSL3	Q8dsl3 human immun
43	38	55.1	759	4 Q9BVH6	Q9bvh6 homo sapien
44	38	55.1	864	5 Q62582	Q62582 encephalito
45	38	55.1	864	5 Q8SRG3	Q8srg3 encephalito

ALIGNMENTS

RESULT 1

Q8TCD2 ID Q8TCD2 PRELIMINARY; PRT; 711 AA.

AC Q8TCD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lactotransferin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347; AAH22347.1; -
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7BE097C45FAF CRC64;

Query Match 78.3%; Score 54; DB 4; Length 711;
Best Local Similarity 81.8%; Pred. No. 0.21;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQWQRMRKV 11

Db 39 CFQWQRMRKV 49

RESULT 2

Q9UCY5 ID Q9UCY5 PRELIMINARY; PRT; 38 AA.

AC Q9UCY5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin homolog (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 X NCBI_TaxID=9606;
 N [1] _____
 K SEQUENCE FROM N.A.
 P MEDLINE=96061613; PubMed=8551695;
 Q Sato I.;
 R "Characterization of the 84-kDa protein with ABH activity in human
 I seminal plasma.";
 Jpn. J. Legal Med. 49:281-293(1995).
 R HSSP; P02788; 1BXA.
 R InterPro; IPR001156; Transferrin.
 R Pfam; PF00405; transferrin; 1.
 Q SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDDEB CRC64;
 Query Match 72.5%; Score 50; DB 4; Length 38;
 Best Local Similarity 81.8%; Pred. No. 0.058;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Y 2 FQWKRMRKVR 12
 N [1] _____
 C 21 FQWKRMRKVR 31
 N [1] _____
 RESULT 3
 9TR80 PRELIMINARY; PRT; 33 AA.
 D Q9TR80;
 T 01-MAY-2000 (TrEMBLrel. 13, Created)
 T 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 T 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 E Lactoferrin (Fragment).
 S Ovis aries (Sheep).
 C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 C Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 C Bovidae; Caprinae; Ovis.
 X NCBI_TaxID=9940;
 N [1] _____
 P SEQUENCE.
 X MEDLINE=95127729; PubMed=7827104;
 A Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
 L Biochim. Biophys. Acta 1243:25-32(1995).
 R HSSP; O77698; ICE2.
 R InterPro; IPR001156; Transferrin.
 R Pfam; PF00405; transferrin; 1.
 Q SEQUENCE 33 AA; 3914 MW; D1904CAB15A73961 CRC64;
 Query Match 66.7%; Score 46; DB 6; Length 33;
 Best Local Similarity 54.5%; Pred. No. 0.26;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Y 1 CFQWKRMRKVR 11
 N [1] _____
 D 19 CYQWQKMRKL 29
 N [1] _____
 RESULT 4
 93780 PRELIMINARY; PRT; 275 AA.
 D Q93780;
 T 01-FEB-1997 (TrEMBLrel. 02, Created)
 T 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 E F53H4.4 protein.
 N F53H4.4.
 S Caenorhabditis elegans.
 C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 C Rhabditidae; Peloderinae; Caenorhabditis.
 X NCBI_TaxID=6239;
 N [1] _____
 P SEQUENCE FROM N.A.
 A Dobson R.;
 Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RQ EMBL; Z81089; CAB03137.1; -.
 SQ SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
 Query Match 65.2%; Score 45; DB 5; Length 275;
 Best Local Similarity 72.7%; Pred. No. 3.2;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FQWKRMRKVR 12
 N [1] _____
 Db 262 FQWKRMRKVR 272
 N [1] _____
 RESULT 5
 Q986A0 PRELIMINARY; PRT; 205 AA.
 ID Q986A0;
 AC Q986A0;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Pyridoxamine 5'-phosphate oxidase.
 GN MLL7454.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OK NCBI_TaxID=381;
 RN [1] _____
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Ideawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AF003011; BAB53553.1; -.
 DR InterPro; IPR000659; Pyridox_Oxidase.
 DR Pfam; PF01243; Pyridox_Oxidase; 1.
 DR ProDom; PD006312; Pyridox_Oxidase; 1.
 DR TIGSFams; TIGR00558; pdxH; 1.
 DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
 KW Complete proteome.
 SQ SEQUENCE 205 AA; 23300 MW; 0BADE4CD312327EA CRC64;
 Query Match 62.3%; Score 43; DB 16; Length 205;
 Best Local Similarity 58.3%; Pred. No. 5.5;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CFQWKRMRKVR 12
 N [1] _____
 Db 88 CFHWKSLRRQVR 99
 N [1] _____
 RESULT 6
 Q8UHC2 PRELIMINARY; PRT; 206 AA.
 ID Q8UHC2;
 AC Q8UHC2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Pyridoxamine 5'-phosphate oxidase.
 GN PDXH OR ATU0760 OR AGR_C1381.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.

NCBI_TaxID=176299;
[1]
SEQUENCE FROM N.A.
MEDLINE=21608550; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen V., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D.S., Grant C.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley P., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens
C58.";
Science 294:2317-2323 (2001).
[2]
SEQUENCE FROM N.A.
MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Quarillo B., Goldman B.S., Cao Y., Askenazi M., Hailing C., Mullin L.,
Houmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
William C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2323-2328 (2001).
ENBL; A8009043; AAL41776.1; -;
ENBL; A8008009; AAK8569.1; -;
Complete proteome.
SEQUENCE 206 AA; 23720 MW; 3B488AE5307C0C1 CRC64;
Query Match 62.3%; Score 43; DB 16; Length 206;
Best Local Similarity 58.3%; Pred. No. 5.5; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
1 CFQWKEAMRKVR 12
||| :|||
88 CFHWKSLRRQVR 99
||| :|||
ULT 7
RH8
Q92RH8 PRELIMINARY; PRT; 206 AA.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PPMP oxidase) protein
(EC 1.4.3.5).
PDXH OR R00895 OR SMC00069.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
NCBI_TaxID=382;
[1]
SEQUENCE FROM N.A.
MEDLINE=21396507; PubMed=11481430;
STRAIN=1021;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boisard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Fumelle B., Rampsberger U.,
Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
ENBL; AL591785; CAC45467.1; -;
InterPro; IPR000659; Pyridox_oxidase.
Pfam; PF01243; Pyridox_oxidase; 1.
ProDom; PD006312; Pyridox_oxidase; 1.

DR TIGRFAMs; TIGR00558; pdxH; 1.
DR PROSITE; PS01064; PYRIDOX_OXIDASE; UNKNOWN_1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;
Query Match 62.3%; Score 43; DB 16; Length 206;
Best Local Similarity 58.3%; Pred. No. 5.5; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
1 CFQWKEAMRKVR 12
||| :|||
88 CFHWKSLRRQVR 99
||| :|||
RESULT 8
Q8YFK3 PRELIMINARY; PRT; 208 AA.
AC Q8YFK3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5).
ENEL1517.
GN Brucella melitensis.
OS Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatal V., Redkar R.J., Patra G., Mujar C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Kasatkorn R., Kyrides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
RL ENBL; A8009587; AAL52698.1; -;
DR InterPro; IPR000659; Pyridox_oxidase.
DR Pfam; PF01243; Pyridox_oxidase; 1.
DR ProDom; PD006312; Pyridox_oxidase; 1.
DR TIGRFAMs; TIGR00558; pdxH; 1.
DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 208 AA; 23866 MW; CB1F50BC9612DE28 CRC64;
Query Match 62.3%; Score 43; DB 16; Length 208;
Best Local Similarity 58.3%; Pred. No. 5.5; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
1 CFQWKEAMRKVR 12
||| :|||
90 CFHWKSLRRQVR 101
||| :|||
RESULT 9
Q9SWS6 PRELIMINARY; PRT; 1121 AA.
AC Q9SWS6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phycochrome B2.
GN PHYB2.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.

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MEDLINE=99413290; PubMed=10485280;
Kerckhoffs L.H., Kelmenson P.M., Schreuder M.E., Kendrick C.I.,
Kendrick R.E., Hanhart C.J., Koorneef M., Pratt L.H.,
Cordonnier-Pratt M.M.;
"Characterization of the gene encoding the apoprotein of phytochrome
B2 in tomato, and identification of molecular lesions in two mutant
alleles.";
Mol. Gen. Genet. 261:901-907 (1999).
EMBL; AF122901; AAD50631.1; -.
InterPro; IPR002198; ADH short.
InterPro; IPR003594; ATPBind_ATPase.
InterPro; IPR003018; GAF.
InterPro; IPR003661; His_kinA.
InterPro; IPR004359; His_KIN_sig.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS domain.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase_c; 1.
SMART; SM00388; HisKIN; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
TIGRfams; TIGR00229; sensory_box; 2.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
PROSITE; PS00245; PHYTOCHROME_1; 1.
PROSITE; PS00046; PHYTOCHROME_2; 1.
SEQUENCE 1121 AA; 125308 MW; ED9EDA704BB37F27 CRC64;

Query Match 60.9%; Score 42; DB 10; Length 1121;
Best Local Similarity 54.5%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 CFQWKRMRKVR 11
|||
777 CFQWNTAMEKL 787

RESULT 10
74118
Q74118 PRELIMINARY; PRT; 508 AA.
01-NOV-1996 (TREMBlrel. 01, Created)
01-NOV-1996 (TREMBlrel. 01, Last sequence update)
01-DEC-2001 (TREMBlrel. 19, Last annotation update)
Gp105 (Fragment).
ENV.
Human immunodeficiency virus type 2.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11709;
[1]_
SEQUENCE FROM N.A.
STRAIN=HIV2D868;
MEDLINE=94187055; PubMed=8139000;
Grez M., Dietrich U., Balfe P., Von Briesen H., Maniar J.K.,
Mahabre G., Delwart E.L., Mullins J.I., Ruebman-Waigmann H.;
"Genetic analysis of Human immunodeficiency virus type 1 and 2 (HIV-1
and HIV-2) mixed infections in India reveals a recent spread of HIV-1
and HIV-2 from a single ancestor for each of these viruses.";
J. Virol. 68:2161-2168 (1994).
EMBL; U07108; AAA1769.1; -.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
NON_TER 508 AA; 58165 MW; 9B103784A08DCB9C CRC64;

Query Match 59.4%; Score 41; DB 15; Length 508;

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MEDLINE=99413290; PubMed=10485280;
Kerckhoffs L.H., Kelmenson P.M., Schreuder M.E., Kendrick C.I.,
Kendrick R.E., Hanhart C.J., Koorneef M., Pratt L.H.,
Cordonnier-Pratt M.M.;
"Characterization of the gene encoding the apoprotein of phytochrome
B2 in tomato, and identification of molecular lesions in two mutant
alleles.";
Mol. Gen. Genet. 261:901-907 (1999).
EMBL; AF122901; AAD50631.1; -.
InterPro; IPR002198; ADH short.
InterPro; IPR003594; ATPBind_ATPase.
InterPro; IPR003018; GAF.
InterPro; IPR003661; His_kinA.
InterPro; IPR004359; His_KIN_sig.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS domain.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase_c; 1.
SMART; SM00388; HisKIN; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
TIGRfams; TIGR00229; sensory_box; 2.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
PROSITE; PS00245; PHYTOCHROME_1; 1.
PROSITE; PS00046; PHYTOCHROME_2; 1.
SEQUENCE 1121 AA; 125308 MW; ED9EDA704BB37F27 CRC64;

Query Match 60.9%; Score 42; DB 10; Length 1121;
Best Local Similarity 54.5%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 CFQWKRMRKVR 11
|||
777 CFQWNTAMEKL 787

RESULT 10
74118
Q74118 PRELIMINARY; PRT; 508 AA.
01-NOV-1996 (TREMBlrel. 01, Created)
01-NOV-1996 (TREMBlrel. 01, Last sequence update)
01-DEC-2001 (TREMBlrel. 19, Last annotation update)
Gp105 (Fragment).
ENV.
Human immunodeficiency virus type 2.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11709;
[1]_
SEQUENCE FROM N.A.
STRAIN=HIV2D868;
MEDLINE=94187055; PubMed=8139000;
Grez M., Dietrich U., Balfe P., Von Briesen H., Maniar J.K.,
Mahabre G., Delwart E.L., Mullins J.I., Ruebman-Waigmann H.;
"Genetic analysis of Human immunodeficiency virus type 1 and 2 (HIV-1
and HIV-2) mixed infections in India reveals a recent spread of HIV-1
and HIV-2 from a single ancestor for each of these viruses.";
J. Virol. 68:2161-2168 (1994).
EMBL; U07108; AAA1769.1; -.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
NON_TER 508 AA; 58165 MW; 9B103784A08DCB9C CRC64;

Query Match 59.4%; Score 41; DB 15; Length 508;

Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QWKRMRKVR 12
:|||||
DB 340 KWKRMRKVR 349

RESULT 11
017772
ID 017772 PRELIMINARY; PRT; 1391 AA.
AC 017772
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F09C3.1 protein.
GN F09C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peleoderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Lennard N.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RV [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; Z92781; CAB07179.2; -.
DR InterPro; IPR001715; Galponin-like.
DR InterPro; IPR000048; IQ region.
DR InterPro; IPR001936; RasGAP.
DR InterPro; IPR000593; RasGAP_C.
DR Pfam; PF00612; IQ; 1.
DR ProDom; PD008735; RasGAP_C; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00015; IQ; 1.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
SQ SEQUENCE 1391 AA; 159210 MW; 794DF9EBFA2B65AC CRC64;

Query Match 59.4%; Score 41; DB 5; Length 1391;
Best Local Similarity 70.0%; Pred. No. 83;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 QWKRMRKVR 12
:|||||
DB 122 QWRMRKVR 131

RESULT 12
Q9XFD5
ID Q9XFD5 PRELIMINARY; PRT; 105 AA.
AC Q9XFD5;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=PANICLE;
RA Liu J., Yang J.;
RT "Suppression subtractive hybridization (SSH) identified candidate
genes that are differentially expressed at rice young panicle.";

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Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL: AF140486; AAD29699.1; -
 InterPro: IPR001128; Cytochrome_P450.

Pfam: PF00067; P450; 1.
 PRINTS: PR00385; P450.

PROSITE: PS00086; CYTOCHROME P450; UNKNOWN_1.
 Heme; Monooxygenase; Oxidoreductase.

NON_TER 1
 SEQUENCE 105 AA; 11912 MW; BOEFCDD487E19F9 CRC64;

Query Match 58.0%; Score 40; DB 10; Length 105;
 Best Local Similarity 60.0%; Pred. No. 9.6;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 CFQWKRAMRK 10
 |||||:|

61 CFQWERLGKK 70
 |||||:|

RESULT 13

00827 PRELIMINARY; PRT; 126 AA.

090827; MEDLINE=97255645; PubMed=9100992;

01-NOV-1998 (TrEMBLrel. 08, Created)
 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 Envelope protein (Fragment).

ENV.

Human immunodeficiency virus type 2.
 Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11709;
 [1]

SEQUENCE FROM N.A.

STRAIN-A; MEDLINE=97255645; PubMed=9100992;

Xiang Z., Ariyoshi K., Wilkins A., Dias F., Whittle H., Breuer J.;
 "HIV type 2 pathogenicity is not related to subtype in rural guinea
 bissau."

AIDS Res. Hum. Retroviruses 13:501-505(1997).
 [2]

SEQUENCE FROM N.A.

STRAIN-A; MEDLINE=98406190; PubMed=9733826;

Grassly N., Xiang Z., Ariyoshi K., Aaby P., Jensen H., Dias F.,
 Van der Loeff, Whittle H., Breuer J.;

"Mortality among human immunodeficiency virus type 2-positive
 villagers in rural guinea-bissau is correlated with viral genotype."

J. Virol. 72:7895-7899(1998).
 EMBL: AJ011269; CAA09580.1; -

InterPro: IPR000777; GPI20.
 Pfam: PF00516; GPI20; 1.

AIDS; Coat protein; Glycoprotein.
 NON_TER 1

NON_TER 126
 SEQUENCE 126 AA; 14891 MW; 248828768F66F88B CRC64;

Query Match 58.0%; Score 40; DB 15; Length 126;
 Best Local Similarity 60.0%; Pred. No. 12;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

3 QWKRAMRKVR 12
 |||||:|

72 EWRKAMQEVK 81
 |||||:|

RESULT 14

IXHP1

09XHP1 PRELIMINARY; PRT; 148 AA.

09XHP1; MEDLINE=98406190; PubMed=9733826;

01-NOV-1999 (TrEMBLrel. 12, Created)
 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE 2S albumin.
 OS Sesamum indicum (Oriental sesame) (Gingelly).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
 OX NCBI_TaxID=4182;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN-TAINAN 1;
 RX MEDLINE=20074970; PubMed=10606554;

RA Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;
 "Molecular cloning of 11S globulin and 2S albumin, the two major seed
 storage proteins in sesame."

RL J. Agric. Food Chem. 47:4932-4938(1999).
 DR EMBL: AF091841; AAD42943.1; -

DR InterPro: IPR003612; NAFIN.
 DR InterPro: IPR000617; Nafin.

DR Pfam: PF00234; tryp_alpha_aml; 1.
 DR PRINTS: PR00496; NAFIN.

DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;

Query Match 58.0%; Score 40; DB 10; Length 148;
 Best Local Similarity 66.7%; Pred. No. 14;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWKRAMR 9
 |||||:|

Db 54 CQWVRSMR 62
 |||||:|

RESULT 15

Q36M21

ID Q96W21 PRELIMINARY; PRT; 274 AA.

AC Q96M21; DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE CDNA FLJ32891 fis, clone TEST12004929.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]

SEQUENCE FROM N.A.

RC TISSUE=TESTIS;

RA Oshima A., Takahashi-Fujii A., Tanase T., Inose N., Takeuchi K.,
 RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,

RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,

RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,

RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
 "NDO human cDNA sequencing project."

RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AK057453; BAB71493.1; -

SQ SEQUENCE 274 AA; 30083 MW; 1DD43654D4135B2F CRC64;

Query Match 58.0%; Score 40; DB 4; Length 274;
 Best Local Similarity 50.0%; Pred. No. 25;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWKRAMRKVR 12
 |||||:|

Db 66 CFQWVGVRVYLR 77
 |||||:|

Search completed: February 21, 2003, 08:00:46
 Job time : 22.6744 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:37:21 ; Search time 28.093 Seconds
(without alignments)
56.918 Million cell updates/sec

Title: 'US-09-743-107B-94
Perfect score: 70
Sequence: 1 CFAWRNMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT*
5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT*
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT*
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT*
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT*
9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT*
10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT*
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT*
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT*
16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT*
17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT*
18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	12	21	AAV78094
2	66	94.3	12	21	AAV78070
3	65	92.9	12	21	AAV78091
4	65	92.9	12	21	AAV78092
5	61	87.1	12	21	AAV78038
6	61	87.1	12	21	AAV78046
7	61	87.1	12	21	AAV78047
8	61	87.1	12	21	AAV78084
9	61	87.1	12	21	AAV78037
10	61	87.1	13	21	AAV78048

11	61	87.1	13	21	AAV78049	Human lactoferrin
12	61	87.1	14	21	AAV78036	Human lactoferrin
13	61	87.1	14	21	AAV78050	Human lactoferrin
14	61	87.1	14	21	AAV78051	Human lactoferrin
15	61	87.1	15	17	AAV78054	Peptide for anti-u
16	61	87.1	15	21	AAV78035	Human lactoferrin
17	61	87.1	15	21	AAV78062	Human lactoferrin
18	61	87.1	15	21	AAV78063	Human lactoferrin
19	61	87.1	16	21	AAV78031	Human lactoferrin
20	61	87.1	16	21	AAV78064	Human lactoferrin
21	61	87.1	16	21	AAV78065	Human lactoferrin
22	61	87.1	17	21	AAV78034	Human lactoferrin
23	61	87.1	17	21	AAV78066	Human lactoferrin
24	61	87.1	17	21	AAV78067	Human lactoferrin
25	61	87.1	18	15	AAV69352	Human lactoferrin
26	61	87.1	18	15	AAV69352	Advanced glycosyla
27	61	87.1	18	17	AAV13397	Human lactoferrin
28	61	87.1	19	21	AAV68867	Human lactoferrin
29	61	87.1	19	21	AAV78032	Amino acid sequenc
30	61	87.1	20	13	AAV21810	Human lactoferrin
31	61	87.1	20	14	AAV44841	Anti microbial pep
32	61	87.1	20	15	AAV48530	Lactoferrin-relate
33	61	87.1	20	15	AAV48531	Lactoferrin-derive
34	61	87.1	20	15	AAV57461	Lactoferrin-derive
35	61	87.1	20	15	AAV57462	Lactoferrin-derive
36	61	87.1	20	16	AAV84698	Bovine lactoferrin
37	61	87.1	20	16	AAV84699	Bovine lactoferrin
38	61	87.1	20	16	AAV80263	Anti-parasitic lac
39	61	87.1	20	16	AAV80264	Anti-parasitic lac
40	61	87.1	20	17	AAV98553	Peptide for anti-u
41	61	87.1	20	17	AAV98552	Lactoferrin-derive
42	61	87.1	20	17	AAV03045	Lactoferrin-derive
43	61	87.1	20	17	AAV90607	Lactoferrin-derive
44	61	87.1	20	17	AAV87621	Lactoferrin-derive
45	61	87.1	20	17	AAV87622	Lactoferrin-derive

ALIGNMENTS

RESULT 1
AAV78094
ID AAV78094 standard; Peptide; 12 AA.
XX AAV78094;
XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:94.
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX Homo sapiens.
XX OS Synthetic.
XX WO200001730-A1.
XX 13-JAN-2000.
XX 06-JUL-1999; 99WO-SE01230.
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX
PS Claim 22; Page 38; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 12 AA;
Query Match 100.0%; Score 70; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CFAWKRNMRKVR 12
DB 1 CFAWKRNMRKVR 12
|||||
RESULT 2
AAY78070
ID AAY78070 standard; Peptide; 12 AA.
XX
AC AAY78070;
XX
DT 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:70.
DE Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
PN 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX
PS Claim 22; Page 35; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
XX SQ Sequence 12 AA;
Query Match 94.3%; Score 66; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00014;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 CFAWKRNMRKVR 12
DB 1 CFAWKRNMRKVR 12
|||||
RESULT 3
AAY78091
ID AAY78091 standard; Peptide; 12 AA.
XX
AC AAY78091;
XX
DT 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:91.
DE Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001730-A1.
PN 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
XX (ASCI-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
XX
PS Claim 22; Page 38; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

aps 0;

lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and *Candida* infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.

QY 1 CFAWKNNRKVR 12
DB 1 CFQWQNNRKVR 12

RESULT 6

AAV78046
ID AAY78046 standard; Peptide; 12 AA.
XX
AC AAY78046;
XX
DT 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:46.
DE
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
PN 13-JAN-2000.
XX
PD 06-JUL-1999; 99WO-SE01230.
XX
PF 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX
PA (ASCI-) A+ SCI INVEST AB.
XX
PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
DR
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
PS Claim 15; Page 35; 102pp; English.
XX

AAV78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumors. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.

XX Sequence 12 AA;

Query Match 87.1%; Score 61; DB 21; Length 12;
Best Local Similarity 83.3%; Pred. NO. 0.00095;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWKNNRKVR 12
DB 1 CFQWQNNRKVR 12

RESULT 7

AAV78047

ID AAY78047 standard; Peptide; 12 AA.
XX
AC AAY78047;

DT 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:47.

DE
XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX

OS Homo sapiens.
OS Synthetic.

XX WO200001730-A1.

PN 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

DR
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -

PS Claim 18; Page 73; 102pp; English.

AAV78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumors. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.

XX Sequence 12 AA;

Query Match 87.1%; Score 61; DB 21; Length 12;
Best Local Similarity 83.3%; Pred. NO. 0.00095;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWKNNRKVR 12

DB 1 CFQWQNNRKVR 12

RESULT 8

AAV78084

ID AAY78084 standard; Peptide; 12 AA.

XX AAY78084;

AC AAY78084;

XX 25-APR-2000 (first entry)

DT Human lactoferrin derived peptide SEQ ID NO:84.

DE

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 PA (ASCI-) A+ SCI INVEST AB.
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 15; Page 74; 102pp; English.
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 13 AA;
 Query Match 87.1%; Score 61; DB 21; Length 13;
 Best Local Similarity 83.3%; Pred. No. 0.001;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFAWKNNRKVR 12
 Db 2 CFQWQRNKRVR 13
 RESULT 11
 AAY78049
 ID AAY78049 standard; Peptide; 13 AA.
 AC AAY78049;
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:49.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2000001730-A1.
 FN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX Claim 18; Page 74; 102pp; English.
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX SQ Sequence 13 AA;
 Query Match 87.1%; Score 61; DB 21; Length 13;
 Best Local Similarity 83.3%; Pred. No. 0.001;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFAWKNNRKVR 12
 Db 2 CFQWQRNKRVR 13
 RESULT 12
 AAY78036
 ID AAY78036 standard; Peptide; 14 AA.
 AC AAY78036;
 DT 25-APR-2000 (first entry)
 XX Human lactoferrin derived peptide SEQ ID NO:36.
 DE Human; lactoferrin; modification; infection; inflammation; tumour;
 XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2000001730-A1.
 FN 13-JAN-2000.
 PD 06-JUL-1999; 99WO-SE01230.
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX (ASCI-) A+ SCI INVEST AB.
 PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX

PS Claim 12; Page 69; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 14 AA;

SQ Query Match 87.1%; Score 61; DB 21; Length 14;

Best Local Similarity 83.3%; Pred. No. 0.0011;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNMKVR 12

DB 3 CFQWQNNMKVR 14

RESULT 13

AA78050

ID AAY78050 standard; Peptide; 14 AA.

XX AC AAY78050;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:50.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;

XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

XX KW urinary tract infection; colitis; Candida infection; fungicidal;

XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX DR New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 15; Page 75; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would

CC enable them to be used for the same purposes as lactoferrin at lower

CC cost.

XX Sequence 14 AA;

SQ Query Match 87.1%; Score 61; DB 21; Length 14;

Best Local Similarity 83.3%; Pred. No. 0.0011;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNMKVR 12

DB 3 CFQWQNNMKVR 14

RESULT 14

AA78051

ID AAY78051 standard; Peptide; 14 AA.

XX AC AAY78051;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:51.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;

XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

XX KW urinary tract infection; colitis; Candida infection; fungicidal;

XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX DR New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 75; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through

CC binding to specific lactoferrin receptors and are then transported

CC through the circulation. A medicinal product of the peptide or fragment

CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal

CC membrane), inflammations and/or tumours. The peptides can also be used

CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.

CC Even though native human lactoferrin have been shown to have desired

CC anti-inflammatory anti-infectious and anti-tumoural properties they

CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX
SQ Sequence 14 AA;

Query Match 87.1%; Score 61; DB 21; Length 14;
Best Local Similarity 83.3%; Pred. No. 0.0011;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNNRKVR 12
|||:|||||
DB 3 CFQWQRNNRKVR 14

RESULT 15

AAR98554
ID AAR98554 standard; Peptide; 15 AA.

XX
AC AAR98554;

DT 12-NOV-1996 (first entry)

DE Peptide for anti-ulcer agent.

KW anti-ulcer agent; low toxicity; stable; heat-resistant.

OS Synthetic.

XX JP08143468-A.

XX 04-JUN-1996.

XX 17-NOV-1994; 94JP-0283869.

XX 17-NOV-1994; 94JP-0283869.

XX (MORG) MORINAGA MILK IND CO LTD.

XX WPI; 1996-318857/32.

PT Anti-ulcer agent contg. peptide - has low toxicity, is
PT heat-resistant and water-soluble

XX Claim 1; Page 11; 11pp; Japanese.

CC AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
CC in toxicity, is heat-resistant and stable in aqueous soln.. It can be
CC administered orally and be produced in large amounts.

SQ Sequence 15 AA;

Query Match 87.1%; Score 61; DB 17; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.0012;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFQWQRNNRKVR 12
|||:|||||
DB 2 CFQWQRNNRKVR 13

Search completed: February 21, 2003, 07:56:44
Job time : 28.093 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds
(without alignments)
39.537 Million cell updates/sec

Title: US-09-743-107B-94
Perfect score: 70
Sequence: 1 CFAWRNMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	87.1	18	1	US-08-204-487-3
2	61	87.1	18	2	US-08-485-948-8
3	61	87.1	18	2	US-08-628-380-8
4	61	87.1	18	2	US-08-475-055-8
5	61	87.1	20	1	US-07-755-161A-3
6	61	87.1	20	1	US-07-891-174-3
7	61	87.1	20	1	US-08-204-487-1
8	61	87.1	20	1	US-08-256-771-24
9	61	87.1	20	1	US-08-256-771-25
10	61	87.1	20	1	US-08-381-984-24
11	61	87.1	20	1	US-08-381-984-25
12	61	87.1	22	4	US-09-508-734-4
13	61	87.1	24	4	US-09-508-734-6
14	61	87.1	25	1	US-07-755-161A-10
15	61	87.1	25	1	US-07-891-174-10
16	61	87.1	25	1	US-08-204-487-7
17	61	87.1	29	4	US-09-508-734-8
18	61	87.1	36	1	US-07-755-161A-8
19	61	87.1	36	1	US-07-891-174-8
20	61	87.1	36	1	US-08-256-771-30
21	61	87.1	36	1	US-08-381-984-29
22	61	87.1	47	2	US-08-484-182A-6
23	61	87.1	47	2	US-08-484-182A-7
24	61	87.1	50	2	US-08-693-274A-7
25	61	87.1	52	4	US-09-017-043A-3
26	61	87.1	53	2	US-08-464-182A-5
27	61	87.1	53	2	US-08-406-271-5

28	61	87.1	54	2	US-08-464-182A-2	Sequence 2, Appli
29	61	87.1	54	2	US-08-406-271-2	Sequence 2, Appli
30	61	87.1	594	3	US-08-724-586-2	Sequence 2, Appli
31	61	87.1	694	4	US-09-421-632-2	Sequence 2, Appli
32	61	87.1	694	4	US-09-932-190-2	Sequence 2, Appli
33	61	87.1	705	2	US-08-655-640-2	Sequence 2, Appli
34	61	87.1	708	2	US-08-655-640-4	Sequence 2, Appli
35	61	87.1	711	1	US-08-154-019-4	Sequence 4, Appli
36	61	87.1	711	1	US-08-461-333-4	Sequence 4, Appli
37	61	87.1	711	3	US-08-464-167-4	Sequence 4, Appli
38	61	87.1	711	3	US-08-158-313-4	Sequence 4, Appli
39	61	87.1	711	4	US-08-476-798-4	Sequence 4, Appli
40	58	82.9	711	1	US-08-145-681-2	Sequence 2, Appli
41	58	82.9	711	1	US-08-250-308-2	Sequence 2, Appli
42	58	82.9	711	1	US-08-453-703-2	Sequence 2, Appli
43	58	82.9	711	2	US-08-456-106-2	Sequence 2, Appli
44	58	82.9	711	3	US-08-456-108-2	Sequence 2, Appli
45	58	82.9	711	4	US-09-265-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/082044487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOIKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: RJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 87.1%; Score 61; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00072;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWKNNRKVR 12
|||:|||||
Db 1 CFQWQNNRKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882

GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 87.1%; Score 61; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00072;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWKNNRKVR 12
|||:|||||
Db 1 CFQWQNNRKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341

GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 05/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-C1, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

US-08-628-380-8

Query Match 87.1%; Score 61; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00072;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWKNNRKVR 12
|||:|||||
Db 1 CFQWQNNRKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245

GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC Compatible
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475,055
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/485,948
;; FILING DATE:
;; APPLICATION NUMBER: 08/488,217
;; FILING DATE: JUNE 7, 1995
;; APPLICATION NUMBER: 08/418,642
;; FILING DATE: APRIL 7, 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 947-1-008A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; DESCRIPTION: LF-cl, 8-25
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
US-08-475-055-8

Query Match 87.1%; Score 61; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00072;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWKRNMRKVR 12
DB 1 CFWQNRNMRKVR 12

RESULT 5
US-07-755-161A-3
; Sequence 3, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: DisplayWrite
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/755,161A
;; FILING DATE: 19910905
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX: 202-371-8856
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 2
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 19"
;; FEATURE:
;; NAME/KEY: modified site
;; LOCATION: 19
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: /note= "thiol group of
;; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
;; OTHER INFORMATION: thiol group of Cys residue at location 2"
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 87.1%; Score 61; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 0.00079;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPWQNNRMRKV 12
DB 2 CFQWQNNRMRKV 13

RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: MATSUDA TOMIYA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site

; LOCATION: 2
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 19"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 19
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond wit
; OTHER INFORMATION: thiol group of Cys residue at location 2"
; PUBLICATION INFORMATION:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; FILING DATE:
; DOCUMENT NUMBER:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 87.1%; Score 61; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.00079;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPWQNNRMRKV 12
DB 2 CFQWQNNRMRKV 13

RESULT 7
US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOIKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGERU
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOPERRIN"
US-08-204-487-1

Query Match 87.1%; Score 61; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.00079;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWKNNMKVR 12
|||:|||||
Db 2 CFQWQNNMKVR 13

RESULT 8
US-08-256-771-24
; Sequence 24, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"

US-08-256-771-24

Query Match 87.1%; Score 61; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.00079;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWKNNMKVR 12
|||:|||||
Db 2 CFQWQNNMKVR 13

RESULT 9
US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25

Query Match 87.1%; Score 61; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.00079;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWKNNMKVR 12
|||:|||||
Db 2 CFQWQNNMKVR 13

RESULT 10
US-08-381-984-24

; Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at positions 2
; OTHER INFORMATION: and 19 are bonded by disulfide linkage"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof"
; US-08-381-984-24
Query Match 87.1%; Score 61; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.00079;
Matches 10; Conservative 1; Mismatches 0; Gaps 0;
QY 1 CFAWKRNMRKVR 12
DB 2 CFQWQRNMRKVR 13
RESULT 11
US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment the
; US-08-381-984-25
Query Match 87.1%; Score 61; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.00079;
Matches 10; Conservative 1; Mismatches 0; Gaps 0;
QY 1 CFAWKRNMRKVR 12
DB 2 CFQWQRNMRKVR 13
RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast a
; TITLE OF INVENTION: useful microorganism thereof
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: FCI/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 4

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; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4

Query Match      87.1%; Score 61; DB 4; Length 22;
Best Local Similarity 83.3%; Pred. No. 0.00086;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWKNNRKVR 12
Db 2 CFWQWRNNRKVR 13

RESULT 13
US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6

Query Match      87.1%; Score 61; DB 4; Length 24;
Best Local Similarity 83.3%; Pred. No. 0.00093;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWKNNRKVR 12
Db 3 CFWQWRNNRKVR 14

RESULT 14
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500KB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHEetical:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10

Query Match      87.1%; Score 61; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 0.00097;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWKNNRKVR 12
Db 4 CFWQWRNNRKVR 15
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```
RESULT 15
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 23-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-891-174-10
; Query Match 87.1%; Score 61; DB 1; Length 25;
; Best Local Similarity 83.3%; Pred.No. 0.00097;
; Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
; QY 1 CFWKNNMKVR 12
; DB 4 CFQWQNNMKVR 15
; Search completed: February 21, 2003, 08:04:27
; Job time : 8.93023 secs
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APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match 87.1%; Score 61; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 0.00043;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNMKVR 12
|||:|||||
Db 3 CFQWQNNMKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Krugel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-023-096-2

Query Match 87.1%; Score 61; DB 9; Length 694;
Best Local Similarity 83.3%; Pred. No. 0.01; Indels 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQWQNNMKVR 12
|||:|||||
Db 22 CFQWQNNMKVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINER (RNSON
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match 75.7%; Score 53; DB 9; Length 15;
Best Local Similarity 75.0%; Pred. No. 0.0056;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQNNMKVR 12
|||:|||||
Db 3 CFQWQNNMKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINER (RNSON
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

Query Match 62.9%; Score 44; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.16;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWKRNKRV 11
|:|:|:|:
Db 3 CYQWQRMEKL 13

RESULT 6

US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US2003002821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVINBU (RMSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/G899/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: G89818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 62.9%; Score 44; DB 9; Length 25;
Best Local Similarity 54.5%; Pred. No. 0.28;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWKRNKRV 11
|:|:|:|:
Db 3 CYQWQRMEKL 13

RESULT 7

US-09-796-753-26
; Sequence 26, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 26
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Mouse
US-09-796-753-26

Query Match 58.6%; Score 41; DB 9; Length 333;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWKRNKRV 11
|:|:|:|:
Db 48 CYGWRNKNKV 58

RESULT 8

US-10-080-960-11
; Sequence 11, Application US/10080960
; Publication No. US20020197695A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 80090, 52874, 52880, 63497, AND 33425
; FILE REFERENCE: 38155-20044.00
; CURRENT APPLICATION NUMBER: US/10/080,960
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/242,040
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/242,038
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,992
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/242,637
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-080-960-11

Query Match 57.1%; Score 40; DB 9; Length 301;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFAWKR 6
| | | | |
DB 296 CFAWKR 301

RESULT 9

US-09-948-078-2
; Sequence 2, Application US/09948078
; Patent No. US20020147308A1
; GENERAL INFORMATION:
; APPLICANT: HOLLOWAY, James L.
; APPLICANT: LOK, Si
; TITLE OF INVENTION: Human Vomeronasal Receptor
; FILE REFERENCE: 00-73
; CURRENT APPLICATION NUMBER: US/09/948,078
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-948-078-2

Query Match 57.1%; Score 40; DB 10; Length 302;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFAWKR 6
| | | | |
DB 297 CFAWKR 302

RESULT 10

US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 55.7%; Score 39; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWKNNRKY 11
| | | | |
DB 3 CLRQWNERKY 13

RESULT 11

US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 55.7%; Score 39; DB 9; Length 25;
Best Local Similarity 54.5%; Pred. No. 1.9;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWKNNRKY 11
| | | | |
DB 3 CLRQWNERKY 13

RESULT 12

US-09-978-295A-119
; Sequence 119, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30

1 PRIOR APPLICATION NUMBER: 60/062250
2 PRIOR FILING DATE: 1997-10-17
3 PRIOR APPLICATION NUMBER: 60/064249
4 PRIOR FILING DATE: 1997-11-03
5 PRIOR APPLICATION NUMBER: 60/065311
6 PRIOR FILING DATE: 1997-11-13
7 PRIOR APPLICATION NUMBER: 60/066364
8 PRIOR FILING DATE: 1997-11-21
9 PRIOR APPLICATION NUMBER: 60/077450
10 PRIOR FILING DATE: 1998-03-10
11 PRIOR APPLICATION NUMBER: 60/077632
12 PRIOR FILING DATE: 1998-03-11
13 PRIOR APPLICATION NUMBER: 60/077641
14 PRIOR FILING DATE: 1998-03-11
15 PRIOR APPLICATION NUMBER: 60/077649
16 PRIOR FILING DATE: 1998-03-11
17 PRIOR APPLICATION NUMBER: 60/077791
18 PRIOR FILING DATE: 1998-03-12
19 PRIOR APPLICATION NUMBER: 60/078004
20 PRIOR FILING DATE: 1998-03-13
21 PRIOR APPLICATION NUMBER: 60/078886
22 PRIOR FILING DATE: 1998-03-20
23 PRIOR APPLICATION NUMBER: 60/078936
24 PRIOR FILING DATE: 1998-03-20
25 PRIOR APPLICATION NUMBER: 60/078910
26 PRIOR FILING DATE: 1998-03-20
27 PRIOR APPLICATION NUMBER: 60/078939
28 PRIOR FILING DATE: 1998-03-20
29 PRIOR APPLICATION NUMBER: 60/079294
30 PRIOR FILING DATE: 1998-03-25
31 PRIOR APPLICATION NUMBER: 60/079656
32 PRIOR FILING DATE: 1998-03-26
33 PRIOR APPLICATION NUMBER: 60/079664
34 PRIOR FILING DATE: 1998-03-27
35 PRIOR APPLICATION NUMBER: 60/079689
36 PRIOR FILING DATE: 1998-03-27
37 PRIOR APPLICATION NUMBER: 60/079663
38 PRIOR FILING DATE: 1998-03-27
39 PRIOR APPLICATION NUMBER: 60/079728
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41 PRIOR APPLICATION NUMBER: 60/079786
42 PRIOR FILING DATE: 1998-03-27
43 PRIOR APPLICATION NUMBER: 60/079920
44 PRIOR FILING DATE: 1998-03-30
45 PRIOR APPLICATION NUMBER: 60/079923
46 PRIOR FILING DATE: 1998-03-30
47 PRIOR APPLICATION NUMBER: 60/080105
48 PRIOR FILING DATE: 1998-03-31
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50 PRIOR FILING DATE: 1998-03-31
51 PRIOR APPLICATION NUMBER: 60/080165
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53 PRIOR APPLICATION NUMBER: 60/080194
54 PRIOR FILING DATE: 1998-03-31
55 PRIOR APPLICATION NUMBER: 60/080327
56 PRIOR FILING DATE: 1998-04-01
57 PRIOR APPLICATION NUMBER: 60/080328
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67 PRIOR APPLICATION NUMBER: 60/081071
68 PRIOR FILING DATE: 1998-04-08
69 PRIOR APPLICATION NUMBER: 60/081195
70 PRIOR FILING DATE: 1998-04-08
71 PRIOR APPLICATION NUMBER: 60/081203
72 PRIOR FILING DATE: 1998-04-09
73 PRIOR APPLICATION NUMBER: 60/081229

74 PRIOR FILING DATE: 1998-04-09
75 PRIOR APPLICATION NUMBER: 60/081955
76 PRIOR FILING DATE: 1998-04-15
77 PRIOR APPLICATION NUMBER: 60/081817
78 PRIOR FILING DATE: 1998-04-15
79 PRIOR APPLICATION NUMBER: 60/081819
80 PRIOR FILING DATE: 1998-04-15
81 PRIOR APPLICATION NUMBER: 60/081952
82 PRIOR FILING DATE: 1998-04-15
83 PRIOR APPLICATION NUMBER: 60/081838
84 PRIOR FILING DATE: 1998-04-15
85 PRIOR APPLICATION NUMBER: 60/082568
86 PRIOR FILING DATE: 1998-04-21
87 PRIOR APPLICATION NUMBER: 60/082569
88 PRIOR FILING DATE: 1998-04-21
89 PRIOR APPLICATION NUMBER: 60/082704
90 PRIOR FILING DATE: 1998-04-22
91 PRIOR APPLICATION NUMBER: 60/082804
92 PRIOR FILING DATE: 1998-04-22
93 PRIOR APPLICATION NUMBER: 60/082700
94 PRIOR FILING DATE: 1998-04-22
95 PRIOR APPLICATION NUMBER: 60/082797
96 PRIOR FILING DATE: 1998-04-22
97 PRIOR APPLICATION NUMBER: 60/082796
98 PRIOR FILING DATE: 1998-04-23
99 PRIOR APPLICATION NUMBER: 60/083336
100 PRIOR FILING DATE: 1998-04-27
101 PRIOR APPLICATION NUMBER: 60/083322
102 PRIOR FILING DATE: 1998-04-28
103 PRIOR APPLICATION NUMBER: 60/083392
104 PRIOR FILING DATE: 1998-04-29
105 PRIOR APPLICATION NUMBER: 60/083495
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108 PRIOR FILING DATE: 1998-04-29
109 PRIOR APPLICATION NUMBER: 60/083499
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115 PRIOR APPLICATION NUMBER: 60/083558
116 PRIOR FILING DATE: 1998-04-29
117 PRIOR APPLICATION NUMBER: 60/083559
118 PRIOR FILING DATE: 1998-04-29
119 PRIOR APPLICATION NUMBER: 60/083500
120 PRIOR FILING DATE: 1998-04-29
121 PRIOR APPLICATION NUMBER: 60/083742
122 PRIOR FILING DATE: 1998-04-30
123 PRIOR APPLICATION NUMBER: 60/084366
124 PRIOR FILING DATE: 1998-05-05
125 PRIOR APPLICATION NUMBER: 60/084414
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130 PRIOR FILING DATE: 1998-05-07
131 PRIOR APPLICATION NUMBER: 60/084639
132 PRIOR FILING DATE: 1998-05-07
133 PRIOR APPLICATION NUMBER: 60/084640
134 PRIOR FILING DATE: 1998-05-07
135 PRIOR APPLICATION NUMBER: 60/084598
136 PRIOR FILING DATE: 1998-05-07
137 PRIOR APPLICATION NUMBER: 60/084600
138 PRIOR FILING DATE: 1998-05-07
139 PRIOR APPLICATION NUMBER: 60/084627
140 PRIOR FILING DATE: 1998-05-07
141 PRIOR APPLICATION NUMBER: 60/084643
142 PRIOR FILING DATE: 1998-05-07
143 PRIOR APPLICATION NUMBER: 60/085339
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146 PRIOR FILING DATE: 1998-05-13

;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 55.7%; Score 39; DB 9; Length 338;
Best Local Similarity 45.5%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAKRNKRV 11
|:|:|:|:
DB 50 CYGMRNSKG 60

RESULT 13

US-09-978-697-119
Sequence 119, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eacon, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364

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;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
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;; PRIOR FILING DATE: 1998-03-31
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;; PRIOR FILING DATE: 1998-03-31
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;; PRIOR FILING DATE: 1998-03-31
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;; PRIOR FILING DATE: 1998-04-01
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;; PRIOR APPLICATION NUMBER: 60/081070
;; PRIOR FILING DATE: 1998-04-08
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;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081071
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081195
;; PRIOR FILING DATE: 1998-04-08
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;; PRIOR APPLICATION NUMBER: 60/081955
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;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Quary Match 55.7%; Score 39; DB 9; Length 338;
Best Local Similarity 45.5%; Pred.No. 23;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAKRNMRKV 11
|:|:|:|:
Db 50 CYGWRNSKGV 60

RESULT 14

US-09-978-192A-119
; Sequence 119, Application US/09978192A
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1998-03-11

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Best Local Similarity 45.5%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 CFAWKNNRKY 11
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RESULT 15
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; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Klijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunes, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; PRIOR FILING DATE: 2001-10-24
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67 PRIOR APPLICATION NUMBER: 60/085704
68 PRIOR FILING DATE: 1998-05-15
69 PRIOR APPLICATION NUMBER: 60/085697

Query Match 55.7%; Score 39; DB 9; Length 338;
Best Local Similarity 45.5%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CFAKNNMKV 11
Db 50 CYGWRNSKGV 50

Search completed: February 21, 2003, 08:11:57
Job time : 6.88372 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 07:48:01; Search time 10.6047 Seconds
(without alignments)
108.784 Million cell updates/sec

Title: US-09-743-107b-94
Perfect score: 70
Sequence: 1 CFAWKRNMRKVR 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	87.1	711	1 THUL	lactotransferrin p
2	46	65.7	511	2 AB0858	hypothetical prote
3	44	62.9	708	2 J02323	lactoferrin - goat
4	43	61.4	393	2 B64639	3-deoxy-manno-octu
5	41	58.6	33	2 S52107	lactoferrin - shee
6	41	58.6	584	2 C84325	hypothetical prote
7	40	57.1	267	2 S77802	hypothetical prote
8	40	57.1	386	2 B82921	serine/threonine k
9	39	55.7	114	2 D33876	carcinoembryonic a
10	39	55.7	121	2 AH3147	hypothetical prote
11	39	55.7	206	2 H97451	pyridoxamine 5'-ph
12	39	55.7	206	2 A82670	probable pyridoxam
13	39	55.7	208	2 AG3441	hypothetical prote
14	39	55.7	275	2 T22597	hypothetical prote
15	39	55.7	282	2 F90580	hypothetical prote
16	39	55.7	393	2 D71876	3-deoxy-manno-octu
17	39	55.7	447	2 T18633	hypothetical prote
18	39	55.7	558	2 T17324	hypothetical prote
19	39	55.7	675	2 S51037	zinc-finger protei
20	39	55.7	707	1 A28438	lactoferrin precu
21	39	55.7	720	2 A36807	hypothetical prote
22	39	55.7	1750	2 H64403	ribonucleoside-tri
23	38	54.3	60	2 A48396	ribosomal protein
24	38	54.3	62	2 AH1301	ribosomal protein
25	38	54.3	62	2 AH1673	ribosomal protein
26	38	54.3	205	2 E30094	26S proteasome SU
27	38	54.3	274	2 B40950	apolipoprotein B-1
28	37	52.9	196	2 T00702	hypothetical prote
29	37	52.9	225	2 S41031	hypothetical prote

30	37	52.9	236	2 A84686	hypothetical prote
31	37	52.9	289	2 G86403	33.3K hypothetical
32	37	52.9	336	1 A39654	cell cycle arrest
33	37	52.9	413	2 T32831	hypothetical prote
34	37	52.9	500	2 G71633	ADP-ATP carrier pr
35	37	52.9	502	2 T01179	hypothetical prote
36	37	52.9	513	2 B86156	T14P4.7 protein -
37	37	52.9	749	2 A45687	outer capsid prote
38	37	52.9	842	2 T04555	hypothetical prote
39	37	52.9	2700	2 D88450	protein F21H11.2 l
40	36.5	52.1	235	2 E91097	hypothetical prote
41	36.5	52.1	235	2 A85943	hypothetical prote
42	36	51.4	116	1 Q0EBHT	hypothetical prote
43	36	51.4	116	2 S09523	merTA protein, 12.
44	36	51.4	236	2 AH0157	probable ribose 5-
45	36	51.4	283	2 G98020	hypothetical prote

ALIGNMENTS

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence, revision 21-Nov-1997 #text change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S

R/Cho. Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AA60324.1; PID:G467237

R/Rev. M.W. Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactof

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:G263311; PIDN:AA624877.1; PID:G263312

A/Experimental source: Placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <ST1>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>


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RESULT 5
S52107
lactoferrin - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C:Accession: S52107
R:Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243: 25-32, 1995
A:Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet a
A:Reference number: S52107; MUID:95127729; PMID:7827104
A:Accession: S52107
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-33 <OIA>
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication

Query Match      58.6%; Score 41; DB 2; Length 33;
Best Local Similarity 45.5%; Pred. No. 1.5;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWKNNRKVR 11
|||:|||||
Db 19 CYQWQKMKRL 29

RESULT 6
C84325
hypothetical protein Vngl732c [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84325
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, F.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: C84325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-584 <STO>
A:Cross-references: GB:AE004437; NID:gl0581192; PIDN:AAG19967.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNGI732C

Query Match      58.6%; Score 41; DB 2; Length 584;
Best Local Similarity 41.7%; Pred. No. 21;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWKNNRKVR 12
|||:|||||
Db 445 CFTWRKDMERKR 456

RESULT 7
S77802
hypothetical protein MC003 - Mycoplasma capricolum (fragment)
C:Species: Mycoplasma capricolum
C:Date: 09-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-Dec-1999
C:Accession: S77802
R:Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;
Mol. Microbiol. 16, 955-967, 1995
A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiolo
A:Reference number: S77739; MUID:96059641; PMID:7476192
A:Accession: S77802
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-267 <BOR>
A:Cross-references: EMBL:Z33006
A:Experimental source: AFCC 27343
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

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C:Genetics:
A:Genetic code: SGC3

Query Match      57.1%; Score 40; DB 2; Length 267;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWKNNRKVR 12
|||:|||||
Db 159 CFGKKNNRQMR 169

RESULT 8
B82921
serine/threonine kinase UU216 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: B82921
R:Glaess, J.I.; Lefkowitz, E.J.; Glass, J.S.; Reiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a n
A:Reference number: A82870
A:Accession: B82921
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-386 <GLA>
A:Cross-references: GB:AE002120; GB:AF222894; NID:g6899167; PIDN:AAF30624.1; GSPDB:GNO
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: pkn; UU216
A:Genetic code: SGC3

Query Match      57.1%; Score 40; DB 2; Length 386;
Best Local Similarity 54.5%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWKNNRKVR 11
|||:|||||
Db 290 CFAWKNNKEDNKL 300

RESULT 9
D33876
carcinoembryonic antigen homolog 4 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jul-1999
C:Accession: D33876
R:Kodellja, V.; Lucas, K.; Barnert, S.; von Kleist, S.; Thompson, J.A.; Zimmermann, W.
J. Biol. Chem. 264, 6906-6912, 1989
A:Title: Identification of a carcinoembryonic antigen gene family in the rat. Analysis
A:Reference number: A33876; MUID:89214106; PMID:2708349
A:Accession: D33876
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <KOD>
A:Cross-references: GB:M60026; NID:g203407; PIDN:AAA0911.1; PID:g554427; GB:J04626; G
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-term

Query Match      55.7%; Score 39; DB 2; Length 114;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWYRGLRKI 11
|||:|||||
Db 42 FAWYRGLRKI 51

RESULT 10
AH3147
hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AH3147

```

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193

A;Accession: AH3147

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-121 <KUR>

A;Cross-references: GB:AE008689; PIDN:RAL45598.1; PID:gl7743317; GSPDB:GN00187

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu4804

A;Map position: linear chromosome

Query Match 55.7%; Score 39; DB 2; Length 121;
Best Local Similarity 54.3%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWKRNMRKV 11

DB 14 CLAWQRNRV 24

RESULT 11

H97451 pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (str

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002

C;Accession: H97451

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, P.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; PMID:11743194

A;Accession: H97451

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-206 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:gl5155733; GSPDB:GN00169

C;Genetics:

A;Gene: AGR_C_1381

A;Map position: circular chromosome

C;Superfamily: pyridoxamine-phosphate oxidase

Query Match 55.7%; Score 39; DB 2; Length 206;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWKRNMRKV 12

DB 88 CFHWKSLRQVR 99

RESULT 12

AB2670 pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Du

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002

C;Accession: AB2670

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193

A;Accession: AB2670

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-206 <KUR>

A;Cross-references: GB:AE008688; PIDN:AAI41776.1; PID:gl7739129; GSPDB:GN00186

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: pdxH

A;Map position: circular chromosome

C;Superfamily: pyridoxamine-phosphate oxidase

Query Match 55.7%; Score 39; DB 2; Length 206;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWKRNMRKV 12

DB 88 CFHWKSLRQVR 99

RESULT 13

AG3441

probable pyridoxamine-phosphate oxidase (BC 1.4.3.5) [imported] - Brucella melitensis

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002

C;Accession: AG3441

R;Delvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujier, C.; Los, T.; Ivanov

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit

A;Reference number: AB3252; PMID:11756688

A;Accession: AG3441

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-208 <KUR>

A;Cross-references: GB:AE008917; PIDN:AAI52698.1; PID:gl7983525; GSPDB:GN00190

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BME11517

A;Map position: I

C;Superfamily: Pyridoxamine-phosphate oxidase

C;Keywords: oxidoreductase

Query Match 55.7%; Score 39; DB 2; Length 208;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWKRNMRKV 12

DB 90 CFHWKSLRQVR 101

RESULT 14

T22597

hypothetical protein F53H4.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C;Accession: T22597

R;Dobson, R.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19587

A;Accession: T22597

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-275 <MIL>

A;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4

A;Experimental source: clone F53H4

C;Genetics:

A;Gene: CESP.F53H4.4

A;Map position: X

A;Introns: 67/1; 153/1

C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4

Query Match 55.7%; Score 39; DB 2; Length 275;
Best Local Similarity 63.6%; Pred. No. 24;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FAWKENMKRV 12
|||:||||
Db 262 FOWKSMKTR 272

RESULT 15
F90580
Hypothetical protein MYPV_5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: F90580
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: F90580
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <KUR>
A:Cross-references: GB:AL445566; PID:G14089965; PIDN:CAC13723.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPV 5500
A:Genetic code: SGC3

Query Match 55.7%; Score 39; DB 2; Length 282;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 FAWKENMKRV 11
|||:||||
Db 20 FAWQNNIKKI 29

Search completed: February 21, 2003, 08:02:48
Job time : 10.6047 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:28:06 ; Search time 5.2093 Seconds
(without alignments)
95.544 Million cell updates/sec

Title: US-09-743-107b-94

Perfect score: 70

Sequence: 1 CFAMKRNMRKV 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues.

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	87.1	711	1 TRFL_HUMAN	P02788 homo sapien
2	44	62.9	708	1 TRFL_CAVDR	Q9tun0 camelus dro
3	44	62.9	708	1 TRFL_CAPHI	Q29477 capra hircu
4	40	57.1	62	1 RL28_THETN	Q8r9u1 theromnaer
5	40	57.1	267	1 Y125_MYCCA	P53661 mycoplasma
6	40	57.1	695	1 TRFL_HORSE	O77811 equus cabal
7	39	55.7	675	1 ZG20_XENLA	P18714 xenopus lae
8	39	55.7	707	1 TRFL_MOUSE	P08071 mus musculu
9	39	55.7	1750	1 Y832_METJA	Q58242 methanococ
10	38	54.3	60	1 RL28_BACST	P23374 bacillus st
11	38	54.3	62	1 RL28_LISMO	Q928j2 listeria mo
12	37	52.9	306	1 BUB2_YEAST	P26448 saccharomyc
13	37	52.9	500	1 TLCE_RICPR	O05962 rickettsia
14	37	52.9	749	1 VP4_ROTGA	Q04916 rotavirus (
15	36	51.4	116	1 MERT_SALTI	P04336 salmonella
16	36	51.4	365	1 LA34_HUMAN	P30453 homo sapien
17	36	51.4	398	1 YK13_CABEL	P34337 caenorhabdi
18	36	51.4	428	1 STL_CHLMU	Q9pj99 chlamydia m
19	35	50.0	421	1 YDT4_SCHPO	O14209 schizosacch
20	35	50.0	480	1 YOS1_CABEL	O09309 caenorhabdi
21	35	50.0	536	1 YEN1_SCHPO	O13695 schizosacch
22	35	50.0	783	1 YNR2_CABEL	Q21988 caenorhabdi
23	34.5	49.3	250	1 FCEA_MOUSE	P20489 mus musculu
24	34.5	49.3	256	1 YQEC_ECOLI	Q46809 escherichia
25	34	48.6	67	1 ATPE_SCHPO	P87316 schizosacch
26	34	48.6	275	1 IL2A_BOVIN	P12342 bos taurus
27	34	48.6	275	1 IL2A_SHEEP	P26898 ovis aries
28	34	48.6	369	1 SP11_MYXVL	P12393 myxoma viru
29	34	48.6	420	1 Y020_BACHD	Q9ka70 bacillus ha
30	34	48.6	428	1 SVH_CHLTR	O84547 chlamydia t
31	34	48.6	485	1 GLG4_BACST	O08328 bacillus st
32	34	48.6	572	1 MAOX_HUMAN	P48163 homo sapien
33	34	48.6	572	1 MAOX_RAT	P13697 rattus norv

ALIGNMENTS

RESULT 1

```

TRFL_HUMAN
ID TRFL_HUMAN STANDARD; PRT; 711 AA.
AC P02788; Q16780; Q16786; Q16789; Q00756; Q9H1Z3; Q96KZ4;
AC Q96KZ5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactoferrin precursor (Lactoferrin) [Contains: Lactoferrin A;
DE Lactoferrin B; Lactoferrin C].
GN LTP OR LP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=9038483; PubMed=2402455;
RT Key M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RL "Complete nucleotide sequence of human mammary gland lactoferrin.";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RL Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Conneely O.M.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang Q., Jimenez-Flores R., Richardson T.;
RL "Molecular cloning and sequence analysis of human lactoferrin.";
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RL "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences.";
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cheng H., Chen X., Huan L.;
RL "cDNA cloning and sequence analysis of human lactoferrin.";
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

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34 34 48.6 1025 1 P021_NASVI
35 34 48.6 1064 1 CYA4_RAT
36 34 48.6 1179 1 ATX1_ARATH
37 34 48.6 1293 1 XPC_DROME
38 34 48.6 1574 1 RPOC_AQUAE
39 34 48.6 1576 1 RPOC_AQUAE
40 34 48.6 1592 1 YHDS_YEAST
41 34 48.6 1696 1 ITN2_HUMAN
42 34 48.6 2273 1 ABCR_HUMAN
43 34 48.6 4568 1 DYHB_CHLRE
44 33.5 47.9 323 1 ATB2_DROME
45 33 47.1 49 1 YIM9_BPH1

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Q03278 nasenia vit
P26770 rattus norv
Q91002 arabidopsis
Q24595 drosofila
O67763 aquifex aeo
Q9x6Y2 aquifex pyr
P38735 saccharomyc
Q9nmz3 homo sapien
P78363 homo sapien
Q39565 chlamydomon
Q24048 drosofila
P10432 bacteriopha

```

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=65104420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
R Legend D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
R Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82626043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
R Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin.";
RL FEBS Lett. 142:107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
R Nian M., Parnell L., Pedria N., Ansari A., Mardis E., Schutz K.,
R Guoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
R Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
R Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
R Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
R Segripani J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker E.N., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=90031861;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
R Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253--methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166329; PubMed=1369293;
RA Tanl F., Ito K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
R Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
R Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
R El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
R Hejtmancik J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR ENBL; X53961; CAA37914.1; -
DR ENBL; U07643; AAB60324.1; -
DR ENBL; M93150; AAA36159.1; -
DR ENBL; M83202; AAA59511.1; -
DR ENBL; M83205; AAA58656.1; -
DR ENBL; M18642; AAA86665.1; -
DR ENBL; AF332168; AAG48753.1; -
DR ENBL; BC015822; AAH15822.1; -
DR ENBL; BC015823; AAH15823.1; -
DR ENBL; M73700; AAA59479.1; -
DR ENBL; X52941; CAA37116.1; -
DR ENBL; U95626; AAB57795.1; -
DR PIR; S11228; TFHUL.
DR PDB; 1LCF; 31-AUG-94.
DR PDB; 1LCT; 31-OCT-93.
DR PDB; 1LFG; 31-JUL-94.
DR PDB; 1LFF; 31-OCT-93.
DR PDB; 1LFI; 31-OCT-93.
DR PDB; 1LGB; 31-AUG-94.
DR PDB; 1LGC; 31-AUG-94.
DR PDB; 1BKA; 08-NOV-96.
DR PDB; 1DSN; 08-MAR-96.
DR PDB; 1HSE; 12-MAR-97.
DR PDB; 1VFD; 21-APR-97.

Query Match 87.1%; Score 61; DB 1; Length 711;
 Best Local Similarity 83.3%; Pred.No. 0.0015;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPWKNRMRKVR 12
 DB 39 CFQWQRMRKVR 50

RESULT 2

TRFL_CAMDR STANDARD; PRT; 708 AA.
 AC QPTUMQ; QWZSS;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R.; Ackermann M.; Farah Z.; Puhar Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin."
 RL Int. Dairy J. 9:481-486 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M.; Srinivasan A.; Singh R.; Sahani M.S.; Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 -!- SUBUNIT: MONOMER (BY SIMILARITY).
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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EMBL; AJ131674; CAB53387.1; -
 DR EMBL; AF165879; AAF82241.1; -
 DR HSSP; 077811; 1BLX.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin.2.
 DR PRINTS; PRO0422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;

Signal.
 FT SIGNAL. 1 19 BY SIMILARITY.
 FT CHAIN 20 708 LACTOTRANSFERRIN.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.
 FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.

FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79
 FT METAL 111 111
 FT METAL 211 211
 FT METAL 272 272
 FT METAL 414 414
 FT METAL 452 452
 FT METAL 545 545
 FT METAL 614 614
 FT BINDING 140 140
 FT BINDING 482 482
 FT CARBOHYD 252 252
 FT CARBOHYD 385 385
 FT CARBOHYD 537 537
 FT CARBOHYD 594 594
 FT CONFLICT 261 261
 FT CONFLICT 304 304
 FT CONFLICT 330 330
 FT CONFLICT 492 494
 FT CONFLICT 506 506
 FT CONFLICT 609 609
 FT CONFLICT 642 642
 FT SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match 62.9%; Score 44; DB 1; Length 708;

Best Local Similarity 58.3%; Pred.No. 1.9;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPWKNRMRKVR 12

DB 38 CAQWQRMRKVR 49

RESULT 3

TRFL_CAMDR STANDARD; PRT; 708 AA.
 ID TRFL_CAMDR Q29477; Q29479;
 AC Q29477; Q29479;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T.; Yu S.; Kim S.; Lee K.; Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=9438004; PubMed=8093048;
 RA le Provost F.; Nocard M.; Guerin G.; Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 syntenic group."
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.

Qy 1 CFAWKRNMRKV 11
| : | : | : | :
Dp 38 CYOWOREMRKL 48

изд. 0. Библиом. 220:307-376 (1994).

U. S. BUREAU OF THE CENSUS (1954).

```

RN RP SEQUENCE OF 85-613 FROM N.A.
RX MEDLINE-90040698; PubMed=2509712;
RA Nicfield W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
RA Poeting A., Knoedel W.;
RT "Second-order repeats in Xenopus laevis finger proteins.";
RJ J. Mol. Biol. 208:639-659(1989).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X82643; CAA57965.1; --
DR PIR; S06565; S06565.
DR HSP; P08046; IALI.
DR TRANSFAC; T02366; --
DR InterPro; IPR000822; Znf C2H2.
DR Pfam; PF00096; zf-C2H2; 18.
DR PRINTS; PR00048; ZINC-FINGER.
DR ProDom; PD000003; Znf C2H2; 5.
DR SMART; SM00355; Znf C2H2; 18.
DR PROSITE; PS00028; ZINC FINGER C2H2 1; 17.
DR PROSITE; PS0157; ZINC FINGER C2H2 2; 18.
KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
FT ZN FING 62 84
FT ZN FING 90 112
FT ZN FING 118 140
FT ZN FING 146 168
FT ZN FING 174 196
FT ZN FING 202 224
FT ZN FING 257 279
FT ZN FING 286 308
FT ZN FING 344 366
FT ZN FING 373 395
FT ZN FING 424 446
FT ZN FING 452 474
FT ZN FING 507 529
FT ZN FING 535 557
FT ZN FING 563 585
FT ZN FING 591 613
FT ZN FING 619 642
SQ SEQUENCE 675 AA; 77116 MW; 033094852C1FCF39 CRC64;
Query Match 55.7%; Score 39; DB 1; Length 675;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 FAWKENM 8
Db 600 FAWKENL 606
RESULT 8
TRFL MOUSE STANDARD; PRT; 707 AA.
ID P08071; P70690; Q61799; Q92222;
AC 01-AUG-1988 (Rel. 08, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactoferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE-87280033; PubMed=3611056;

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RA Pentecost B.T., Teng C.T.;
RT "Lactoferrin is the major estrogen inducible protein of mouse
RT uterine secretions.";
RL J. Biol. Chem. 262:10134-10139(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Moriishi K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE-92042099; PubMed=1939212;
RA Liu Y., Teng C.T.;
RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";
RL J. Biol. Chem. 266:21880-21885(1991).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J03298; AAA40525.1; --
DR EMBL; D88510; BAAL3633.1; --
DR EMBL; BC006904; AAH06904.1; --
DR EMBL; M74778; AAA39427.1; --
DR PIR; A28438; A28438.
DR HSP; P02788; ICB6.
DR MGD; MGI:96837; Ltf.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 707 LACTOTRANSFERRIN.
FT REPEAT 20 357 1.
FT REPEAT 358 707 2.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.
FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 283 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 423 702 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 78 IRON 1 (BY SIMILARITY).
FT METAL 110 110 IRON 1 (BY SIMILARITY).

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FT METAL 210 210 IRON 1 (BY SIMILARITY).
 FT METAL 271 271 IRON 1 (BY SIMILARITY).
 FT METAL 413 413 IRON 2 (BY SIMILARITY).
 FT METAL 451 451 IRON 2 (BY SIMILARITY).
 FT METAL 544 544 IRON 2 (BY SIMILARITY).
 FT METAL 613 613 IRON 2 (BY SIMILARITY).
 FT BINDING 139 139 ANION (POTENTIAL).
 FT BINDING 481 481 ANION (POTENTIAL).
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 1 2 MR -> IOG (IN REF. 1).
 FT CONFLICT 25 25 R -> Q (IN REF. 2).
 FT CONFLICT 82 82 S -> L (IN REF. 2).
 FT CONFLICT 359 359 M -> T (IN REF. 2).
 FT CONFLICT 382 382 A -> D (IN REF. 1).
 FT CONFLICT 449 449 E -> G (IN REF. 2).
 FT CONFLICT 629 629 L -> V (IN REF. 1).
 SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;
 Query Match 55.7%; Score 39; DB 1; Length 707;
 Best Local Similarity 54.5%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CFAWKRMKRV 11
 DB 37 CLRWQNMKRV 47
 RESULT 9
 Y832 METJA STANDARD; PRT; 1750 AA.
 AC Q58242;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ0832 [Contains: Mja rnr-1 intein; Mja rnr-2 intein].
 DE intein].
 GN MJ0832.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hrust M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
 RL Science 273:1058-1073 (1996).
 CC -!- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTNIN) FOLLOWED BY PEPTIDE LIGATION (POTENTIAL).
 CC -!- SIMILARITY: WEAK IN THE C-TERMINAL, TO M.JANNASCHII MJ0885.
 CC -----
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 CC -----
 CC EMBL; U67527; AAB98034.1; .
 CC HSSP; P17255; 1DFA.
 CC TIGR; MJ0832; .

DR InterPro; IPR005144; ATP.
 DR InterPro; IPR003586; Hedgehog_hintc.
 DR InterPro; IPR003587; Hedgehog_hintn.
 DR InterPro; IPR002203; intein.
 DR Pfam; PF03477; ATP-cone; 2.
 DR PRINTS; PRO0379; INTEIN.
 DR SMART; SM00306; HintC; 2.
 DR PROSITE; PS00818; INTEIN_C_TER; 2.
 DR PROSITE; PS00819; INTEIN_ENDONUCLEASE; 2.
 DR PROSITE; PS00817; INTEIN_N_TER; 2.
 KW Hypothetical protein; Autocatalytic cleavage; Protein splicing;
 Complete proteome.
 FT CHAIN 1 337 HYPOTHETICAL PROTEIN MJ0832, 1ST PART (POTENTIAL).
 FT CHAIN 338 790 MJA RNR-1 INTEIN (POTENTIAL).
 FT CHAIN 791 1058 HYPOTHETICAL PROTEIN MJ0832, 2ND PART (POTENTIAL).
 FT CHAIN 1059 1591 MJA RNR-2 INTEIN (POTENTIAL).
 FT CHAIN 1592 1750 HYPOTHETICAL PROTEIN MJ0832, 3RD PART (POTENTIAL).
 SQ SEQUENCE 1750 AA; 203279 MW; 6D6693B770A25359 CRC64;
 Query Match 55.7%; Score 39; DB 1; Length 1750;
 Best Local Similarity 54.5%; Pred. No. 39;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FAWKRMKRV 12
 DB 718 YAWKSNRKVK 728
 RESULT 10
 RL28 BACST STANDARD; PRT; 60 AA.
 ID RL28 BACST
 AC P23374;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L28.
 GN RPMB.
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillales; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92075758; PubMed=1742360;
 RA Kruff V., Kapp U., Wittmann-Liebold B.;
 RT "Characterization and primary structure of proteins L28, L33 and L34 from Bacillus stearothermophilus ribosomes.";
 RL Biochimie 73:855-860 (1991).
 CC -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
 DR PIR; A48396; A48396.
 DR InterPro; IPR001383; Ribosomal_L28.
 DR Pfam; PF00830; Ribosomal_L28; 1.
 DR TIGRFAMs; TIGR00009; L28; 1.
 KW Ribosomal protein.
 FT INIT MET 0
 SQ SEQUENCE 60 AA; 6810 MW; 2AD9161CD60B92F4 CRC64;
 Query Match 54.3%; Score 38; DB 1; Length 60;
 Best Local Similarity 56.7%; Pred. No. 1.8;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 WKBNRMKRV 12
 DB 27 WKANLQKRV 35
 RESULT 11
 RL28 LISMO STANDARD; PRT; 62 AA.
 ID RL28 LISMO

AC Q2AJ2;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L28.
 DE RPMB OR LM01816 OR LIN1930.
 GN Listeria monocytogenes, and
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639, 1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES: *L. monocytogenes*, and *L. innocua*;
 RC STRAIN=BGD-6 / Serovar 1/2a, and CLIP 11262 / Serovar 6a;
 RX MEDLINE=21357279; PubMed=11679669;
 RA Glaser P., Frangeul L., Blochesser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
 RA Domant E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Etienne K.-D., Fsihi H., Garcia-del Portillo P., Garrido P.,
 RA Gautier L., Goshel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkak G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Neelari H.,
 RA Nordieck G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Rammel B., Rose M., Schluter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
 RT "Comparative genomics of *Listeria* species."; Science 294:849-852(2001).
 RL Science 294:849-852(2001).
 CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 CC EMBL; AL591981; CAC99894.1; -;
 DR EMBL; AL596170; CAC97160.1; -;
 DR Listilist; LIN01930; -;
 DR Listilist; LM001816; -;
 DR InterPro; IPR001383; Ribosomal_L28.
 DR Pfam; PF00830; Ribosomal_L28; 1.
 DR TIGRFAMS; TIGR00009; L28; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 62 AA; 6991 MW; AA43DE039213C562 CRC64;
 Query Match 54.3%; Score 38; DB 1; Length 62;
 Best Local Similarity 66.7%; Pred. No. 1.9;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 WKNNRKRVR 12
 DB 29 WKANLQKVR 37
 RESULT 12
 BUB2 YEAST
 ID BUB2 YEAST STANDARD; PRT; 306 AA.
 AC P26448;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitotic checkpoint protein BUB2 (Cell cycle arrest protein BUB2).
 GN BUB2 OR YNR055C OR YMR796.08C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Scharitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;

RX MEDLINE=91330299; PubMed=1651171;
 RA Hoyt M.A., Totis L., Roberts B.T.;
 RT "S. cerevisiae genes required for cell cycle arrest in response to
 RT loss of microtubule function."; Cell 66:507-517(1991).
 RL Cell 66:507-517(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=21385309; PubMed=11493673;
 RA Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Pesquet D.,
 RA Johnston J.H.;
 RT "The BUB2-dependent mitotic pathway in yeast acts every cell cycle and
 RT regulates cytokinesis."; J. Cell Sci. 114:2345-2354(2001).
 RL J. Cell Sci. 114:2345-2354(2001).
 CC -1- FUNCTION: Part of a checkpoint which monitors spindle integrity
 CC and prevents premature exit from mitosis. This cell-cycle arrest
 CC depends upon inhibition of the G-protein Tem1 by the BFA1/BUB2
 CC complex.
 CC -1- SUBUNIT: Interacts with BFA1.
 CC -1- SUBCELLULAR LOCATION: Spindle poles.
 CC -1- SIMILARITY: TO S. POMBE CDC16.
 CC -----
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 CC -----
 CC EMBL; M64706; AAA16885.1; -;
 DR EMBL; Z49703; CAA89765.1; -;
 DR FIR; A39654; A39654.
 DR SGD; S0004659; BUB2.
 DR InterPro; IPR000195; RabGAP_TBC.
 DR Pfam; PF00566; TBC; 1.
 DR SMART; SM00164; TBC; 1.
 KW Cell cycle; Mitosis.
 SQ SEQUENCE 306 AA; 35027 MW; A1DDBF548E81EA3 CRC64;
 Query Match 52.9%; Score 37; DB 1; Length 306;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFAWKENMRK 10
 DB 108 CFAWQIQRR 117
 RESULT 13
 TLCE_RICPR STANDARD; PRT; 500 AA.
 ID TLCE_RICPR STANDARD; PRT; 500 AA.
 AC C059Z2;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP-ATP carrier protein 5 (ADP/ATP translocase 5).
 GN TLCE OR TLC5 OR RP739.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Scharitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;

RT The genome sequence of Rickettsia prowazekii and the origin of
 RL mitochondria." ;
 RL Nature 396:133-140(1998).
 RN [2]
 RP SEQUENCE OF 325-500 FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=97419517; PubMed=9274032;
 RA Andersson J.C., Andersson S.G.E.;
 RT "Genomic rearrangements during evolution of the obligate
 RT intracellular parasite Rickettsia prowazekii as inferred from an
 RT analysis of 52015 bp nucleotide sequence." ;
 RL Microbiology 143:2783-2795(1997).
 CC -!- FUNCTION: PROVIDES THE RICKETTSIAL CELL WITH HOST ATP IN
 CC EXCHANGE FOR RICKETTSIAL ADP. THIS IS AN OBLIGATE EXCHANGE SYSTEM.
 CC THIS ENERGY ACQUIRING ACTIVITY IS AN IMPORTANT COMPONENT OF
 CC RICKETTSIAL PARASITISM (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE ADP/ATP TRANSLOCASE TIC FAMILY.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC EMBL; AJ235273; CAA15167.1; --
 CC EMBL; Y11778; CAA72457.1; --
 DR InterPro; IPR004667; ADP_ATP_car.
 DR Pfam; PF03219; TIC; 1.
 DR TIGRFAMs; TIGR00769; AAA; 1.
 KW Transmembrane; Transport; ATP-binding; Multigene family;
 KW Complete proteome.
 FT TRANSMEM 26 46 POTENTIAL.
 FT TRANSMEM 62 82 POTENTIAL.
 FT TRANSMEM 94 114 POTENTIAL.
 FT TRANSMEM 149 169 POTENTIAL.
 FT TRANSMEM 184 204 POTENTIAL.
 FT TRANSMEM 224 244 POTENTIAL.
 FT TRANSMEM 287 307 POTENTIAL.
 FT TRANSMEM 328 348 POTENTIAL.
 FT TRANSMEM 357 377 POTENTIAL.
 FT TRANSMEM 381 401 POTENTIAL.
 FT TRANSMEM 469 489 POTENTIAL.
 SQ SEQUENCE 500 AA; 57073 MW; FE3DB48D08CF5F72 CRC64;
 Query Match 52.9%; Score 37; DB 1; Length 500;
 Best Local Similarity 54.5%; Pred. No. 25;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFAWKENMEKV 11
 Db 482 CFAWIVYVRKI 492
 RESULT 14
 ID VP4_ROTGA STANDARD; PRT; 749 AA.
 AC Q04916;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
 GN S4.
 OS Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
 OC NCBI_TaxID=12705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9323240; PubMed=8386274;
 RA Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chan G.-M.;
 RT "Identification and baculovirus expression of the VP4 protein of the

RT human group B rotavirus ADRV." ;
 RL J. Virol. 67:2730-2738(1993).
 CC -!- SUBCELLULAR LOCATION: Outer capsid.
 CC -!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M91434; AAA47338.1; --
 DR InterPro; IPR000416; Cap_VP4.
 DR Pfam; PF00426; VP4; 1.
 KW Coat protein; Glycoprotein.
 FT CARBOHYD 29 29
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 568 568 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 681 681 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 698 698 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 749 AA; 84362 MW; D123527DEAE0F21 CRC64;
 Query Match 52.9%; Score 37; DB 1; Length 749;
 Best Local Similarity 50.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CFAWKENMEKV 12
 Db 195 CFTMDMNCANVR 206
 RESULT 15
 ID WEST_SALTI STANDARD; PRT; 116 AA.
 AC P04336;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mercuric transport protein (Mercury ion transport protein).
 GN MERT OR HCM1_234C.
 OS Salmonella typhi and
 OS Shigella flexneri.
 OG Plasmid pHCM1, and Plasmid IncFII NRI.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OC NCBI_TaxID=601, 623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=CT18; PLASMID=pHCM1;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krögh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18." ;
 RL Nature 413:848-852(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri;
 RX MEDLINE=85014891; PubMed=6091128;
 RA Misra T.K., Brown N.L., Fritzinger D.C., Pridmore R.D., Barnes W.M.,

```

RA Haberstroh L., Silver S.;
RT "Mercuric ion-resistance operons of plasmid R100 and transposon
RT Tn501: the beginning of the operon including the regulatory region
RT and the first two structural genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5975-5979 (1984).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; PLASMID=IncFII NR1; TRANSPOSON=Tn21;
RX MEDLINE=85159407; PubMed=6530603;
RA Barrineau P., Gilbert P., Jackson W.J., Jones C.S., Summers A.O.,
RA Wisdom S.;
RT "The DNA sequence of the mercury resistance operon of the IncFII
RT plasmid NR1.";
RL J. Mol. Appl. Genet. 2:601-619 (1984).
CC -1- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION
CC FROM THE PERIPLASMIC MERP PROTEIN TO THE MERCURIC REDUCTASE
CC (NERA)
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AL513383; CAD09816.1; -.
DR EMBL; J01730; AAA92261.1; -.
DR EMBL; K03089; AAB53075.1; -.
DR PIR; A04458; QJEBHT.
DR InterPro; IPR003457; Transprt_Mert.
DR Pfam; PF02411; Mert; 1.
DR Transport; Mercuric resistance; Inner membrane; Mercury; Plasmid;
KW Transmembrane; Transposable element; Complete proteome.
FT TRANSMEM 16 36 POTENTIAL.
FT TRANSMEM 46 66 POTENTIAL.
FT TRANSMEM 94 114 POTENTIAL.
FT METAL 24 24 HG(2+) (POTENTIAL).
FT METAL 25 25 HG(2+) (POTENTIAL).
FT METAL 76 76 HG(2+) (POTENTIAL).
FT METAL 82 82 HG(2+) (POTENTIAL).
SQ SEQUENCE 116 AA; 12521 MW; 8CF0744F4B0F6EE4 CRC64;

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Query Match      51.4%; Score 36; DB 1; Length 116;
Best Local Similarity 53.6%; Pred.No. 8.3;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 2 FAWKKNMKVR 12
   |||||
Db 64 FAWKRIYRPVQ 74

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Search completed: February 21, 2003, 07:51:41
Job time : 6.2093 secs

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
(without alignments)
114.078 Million cell updates/sec

Title: US-09-743-107B-94

Perfect score: 70

Sequence: 1 CFAWKNRKR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	80.0	711	4 Q8TCD2	Q8tcd2 homo sapien
2	52	74.3	38	4 Q9UCY5	Q9ucy5 homo sapien
3	46	65.7	511	16 Q82462	Q82462 salmonella
4	43	61.4	393	16 Q25611	Q25611 helicobacte
5	41	58.6	33	6 Q9TR80	Q9tr80 ovis aries
6	41	58.6	550	11 Q9JUZ5	Q9jjz5 mus musculu
7	41	58.6	584	17 Q9HPA3	Q9hpa3 halobacteri
8	40	57.1	62	16 Q8R9U1	Q8r9u1 thermococae
9	40	57.1	206	4 Q9BXW1	Q9bxw1 homo sapien
10	40	57.1	301	4 Q8TDU2	Q8tdu2 homo sapien
11	40	57.1	374	4 Q60735	Q60735 homo sapien
12	40	57.1	374	4 Q96XW8	Q96xw8 homo sapien
13	40	57.1	374	11 Q9JUX4	Q9jux4 mus musculu
14	40	57.1	386	16 Q9PQS6	Q9pqs6 ureaplasma
15	39	55.7	114	11 Q63104	Q63104 rattus norv
16	39	55.7	121	16 Q8U6K3	Q8u6k3 agrobacteri

17	39	55.7	205	16 Q986A0	Q986a0 rhizobium 1
18	39	55.7	206	16 Q8UHC2	Q8uhc2 agrobacteri
19	39	55.7	206	16 Q92RH8	Q92rh8 rhizobium m
20	39	55.7	208	16 Q8YFK3	Q8yfk3 brucella me
21	39	55.7	234	11 Q63112	Q63112 rattus norv
22	39	55.7	275	5 Q93780	Q93780 caenorhabdi
23	39	55.7	282	16 Q98Q19	Q98q19 mycoplasma
24	39	55.7	341	11 Q8R2A4	Q8r2a4 mus musculu
25	39	55.7	393	16 Q92KP4	Q92kp4 helicobacte
26	39	55.7	447	5 Q17549	Q17549 caenorhabdi
27	39	55.7	519	10 Q93833	Q93833 arabidopsis
28	39	55.7	553	4 Q9NZL7	Q9nzt7 homo sapien
29	39	55.7	554	4 Q9NY67	Q9ny67 homo sapien
30	39	55.7	558	4 Q9UFK6	Q9ufk6 homo sapien
31	39	55.7	720	10 Q9CA22	Q9cac2 arabidopsis
32	38	54.3	81	15 Q90863	Q90863 human immun
33	38	54.3	205	8 Q9ARR2	Q9arr2 guillardi
34	38	54.3	273	2 Q31090	Q31090 rhizobium 1
35	38	54.3	318	2 Q9ADZ8	Q9adz8 agrobacteri
36	38	54.3	886	5 Q9VZV1	Q9vzv1 drosophila
37	37	52.9	196	4 Q14557	Q14557 homo sapien
38	37	52.9	225	5 Q21197	Q21197 caenorhabdi
39	37	52.9	232	4 Q96H38	Q96h38 homo sapien
40	37	52.9	236	10 Q9SK05	Q9sk05 arabidopsis
41	37	52.9	246	4 Q96GY3	Q96gy3 homo sapien
42	37	52.9	289	10 Q9C6N2	Q9c6n2 arabidopsis
43	37	52.9	302	16 Q987S1	Q987s1 rhizobium 1
44	37	52.9	317	5 Q44841	Q44841 caenorhabdi
45	37	52.9	502	10 Q85237	Q85237 arabidopsis

ALIGNMENTS

RESULT 1

Q8TCD2 ID Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC022347; AAH22347.1; -
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7BE097C45FAF CRC64;

Query Match 80.0%; Score 56; DB 4; Length 711;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFAWKNRKR 11

Db 39 CFQWQNRKR 49

RESULT 2

Q9UCY5 ID Q9UCY5 PRELIMINARY; PRT; 38 AA.
AC Q9UCY5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Lactoferrin homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96081613; PubMed=8551595;
RA Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
RL seminal plasma.";
RL Jpn. J. Legal Med. 49:281-293(1995).
RA Flensburg K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodex A.,
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watney L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AF000604; AAD08000.1; -.
DR TIGR; HP0957; -.
KW Hypothetical protein; Transferase; Complete proteome.
SQ SEQUENCE 393 AA; 45622 MW; 6428BA3321554F46 CRC64;

Query Match 61.4%; Score 43; DB 16; Length 393;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 FAWKNNRKR 12
Db 110 FAWKNNRKR 120

RESULT 5
Q9TR80 PRELIMINARY; PRT; 33 AA.
ID Q9TR80
AC Q9TR80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jolles P., Migliore-Samouri D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSP; O7698; 1CB2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAB15A73961 CRC64;

Query Match 58.6%; Score 41; DB 6; Length 33;
Best Local Similarity 45.5%; Pred. No. 2;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWNNRKR 11
Db 19 CYQWQKQKRL 29

RESULT 6
Q9JUZ5 PRELIMINARY; PRT; 550 AA.
ID Q9JUZ5
AC Q9JUZ5;
DT 01-JUN-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 3-deoxy-D-manno-octulosonic-acid transferase (KDTA).
DR HP0957.

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OC Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96081613; PubMed=8551595;
RA Sato I.;
RT "Characterization of the 84-kDa protein with ABH activity in human
RL seminal plasma.";
RL Jpn. J. Legal Med. 49:281-293(1995).
RA Flensburg K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodex A.,
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watney L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AF000604; AAD08000.1; -.
DR TIGR; HP0957; -.
KW Hypothetical protein; Transferase; Complete proteome.
SQ SEQUENCE 393 AA; 45622 MW; 6428BA3321554F46 CRC64;

Query Match 74.3%; Score 52; DB 4; Length 38;
Best Local Similarity 81.8%; Pred. No. 0.026;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FAWKNNRKR 12
Db 21 FAWKNNRKR 31

RESULT 3
Q82462 PRELIMINARY; PRT; 511 AA.
ID Q82462
AC Q82462;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein STV3070.
GN STV3070.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Faltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen I.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627276; CAD06049.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 511 AA; 58126 MW; E2DD124E10D178B CRC64;

Query Match 65.7%; Score 46; DB 16; Length 511;
Best Local Similarity 66.7%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWNNRKR 12
Db 350 CFAWNNRKR 361

RESULT 4
Q25611 PRELIMINARY; PRT; 393 AA.
ID Q25611
AC Q25611;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 3-deoxy-D-manno-octulosonic-acid transferase (KDTA).
DR HP0957.

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OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelsen K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodex A.,
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watney L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AF000604; AAD08000.1; -.
DR TIGR; HP0957; -.
KW Hypothetical protein; Transferase; Complete proteome.
SQ SEQUENCE 393 AA; 45622 MW; 6428BA3321554F46 CRC64;

Query Match 61.4%; Score 43; DB 16; Length 393;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 FAWKNNRKR 12
Db 110 FAWKNNRKR 120

RESULT 5
Q9TR80 PRELIMINARY; PRT; 33 AA.
ID Q9TR80
AC Q9TR80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Lactoferrin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95127729; PubMed=7827104;
RA Qian Z.Y., Jolles P., Migliore-Samouri D., Fiat A.M.;
RL Biochim. Biophys. Acta 1243:25-32(1995).
DR HSP; O7698; 1CB2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
SQ SEQUENCE 33 AA; 3914 MW; D1904CAB15A73961 CRC64;

Query Match 58.6%; Score 41; DB 6; Length 33;
Best Local Similarity 45.5%; Pred. No. 2;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWNNRKR 11
Db 19 CYQWQKQKRL 29

RESULT 6
Q9JUZ5 PRELIMINARY; PRT; 550 AA.
ID Q9JUZ5
AC Q9JUZ5;
DT 01-JUN-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 3-deoxy-D-manno-octulosonic-acid transferase (KDTA).
DR HP0957.

```

DE Hypothetical 61.5 kDa protein.
GN EGF16 OR W60.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Franco B.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20241927; PubMed=10777661;
RA Buchner G., Orfanelli U., Ouadri N., Bassi M.T., Andolfi G.;
RT "Identification of a new EGF-repeat-containing gene from human Xp22:
RT A candidate for developmental disorders.";
RL Genomics 65:16-23(2000).
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL; AJ245672; CAB92138.1; --
DR HSP; P35555; 1EMN.
DR MGD; MGI:1858599; Egf16.
DR InterPro; IPR001152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00629; MAM; 1.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00001; EGF_Like; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS00060; MAM_2; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
KW Hypothetical protein; Repeat.
SQ SEQUENCE 550 AA; 61520 MW; DEF936325C9F31B3 CRC64;
Query Match 58.6%; Score 41; DB 11; Length 550;
Best Local Similarity 56.58; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CFWKRRNRKV 11
Db 48 CYGWRNRKGV 58
RESULT 7
Q9HPA3 PRELIMINARY; PRT; 584 AA.
AC Q9HPA3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Vng1732c.
GN Vng1732c.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Melti R., Goo Y.A.,
RA Leithausser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005078; AAG19967.1; --
DR InterPro; IPR001646; Septide_repeat.
DR InterPro; IPR001622; K-channel_pore.
DR Pfam; PF00805; Pentapeptide; 2.
KW Complete proteome.
SQ SEQUENCE 584 AA; 65151 MW; 21BF5D5F0486CCC6 CRC64;
Query Match 58.6%; Score 41; DB 17; Length 584;
Best Local Similarity 41.7%; Pred. No. 39;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CFWKRRNRKV 12
Db 445 CFTWRKQMRKR 456
RESULT 8
Q8R9U1 PRELIMINARY; PRT; 62 AA.
ID Q8R9U1
AC Q8R9U1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ribosomal protein L28.
GN RMB OR TTE1495.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013107; AAM24713.1; --
KW Complete proteome.
SQ SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
Query Match 57.1%; Score 40; DB 16; Length 62;
Best Local Similarity 77.8%; Pred. No. 5.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 WKRRNRKV 12
Db 28 WKPNRKV 36
RESULT 9
Q9BXW1 PRELIMINARY; PRT; 206 AA.
ID Q9BXW1
AC Q9BXW1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PNAS-125.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Yu W.-Q., Sun B.-Z., Chai Y.-B., Zhu F., Liu X.-S., Li Z., Lu F.,
RA Yan W., Yang H., Zhao Z.-L.;
RT "Human acute promyelocytic leukemia cell line NB4's
RT apoptosis/differentiation related genes.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF271183; AAK07542.1; --
DR InterPro; IPR000717; PCI.

DR Pfam; PF01399; PCI; 1.
DR SMART; SM00088; PINT; 1.
SQ SEQUENCE 206 AA; 23754 MW; 940D5B66271A44B4 CRC64;
Query Match 57.1%; Score 40; DB 4; Length 206;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 AKRNNRKVR 12
DB 172 AKQNLNKVK 181
RESULT 10
Q8TDU2 PRELIMINARY; PRT; 301 AA.
AC Q8TDU2;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Putative G-protein coupled receptor.
GN GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RT "Identification of G protein-coupled receptor genes from the human genome sequence."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL; AB083609; BAB89322.1; -.
KW Receptor.
SQ SEQUENCE 301 AA; 33557 MW; AB7F9792957BFCA6 CRC64;
Query Match 57.1%; Score 40; DB 4; Length 301;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFAWKR 6
DB 296 CFAWKR 301
RESULT 11
O60735 PRELIMINARY; PRT; 374 AA.
AC O60735;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Gal7 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Zhao Z., Huang X., Li N., Zhu X., Cao X.;
RT "A novel gene from human dendritic cell."
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF064603; AAC17108.1; -.
DR InterPro; IPR000717; PCI.
DR Pfam; PF01399; PCI; 1.
DR SMART; SM00088; PINT; 1.
SQ SEQUENCE 374 AA; 42512 MW; 2CFF2BCB70F997A7 CRC64;
Query Match 57.1%; Score 40; DB 4; Length 374;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 AKRNNRKVR 12
DB 356 AKQNLNKVK 365
RESULT 12
Q96KM8 PRELIMINARY; PRT; 374 AA.
AC Q96KM8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE DJ69B10.1 (Gal7 protein) (Hypothetical 42.5 kDa protein).
GN DJ69B10.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cobley V.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL078477; CAC88392.1; -.
DR EMBL; BC019103; AAH19103.1; -.
DR InterPro; IPR000717; PCI.
DR Pfam; PF01399; PCI; 1.
KW Hypothetical protein.
SQ SEQUENCE 374 AA; 42503 MW; 63736CA2B093D794 CRC64;
Query Match 57.1%; Score 40; DB 4; Length 374;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 AKRNNRKVR 12
DB 356 AKQNLNKVK 365
RESULT 13
Q99JX4 PRELIMINARY; PRT; 374 AA.
AC Q99JX4;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Similar to dendritic cell protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005598; AAH05598.1; -.
DR InterPro; IPR000717; PCI.
DR Pfam; PF01399; PCI; 1.
DR SMART; SM00088; PINT; 1.
SQ SEQUENCE 374 AA; 42517 MW; 09845D87E792B783 CRC64;
Query Match 57.1%; Score 40; DB 11; Length 374;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 AKRNNRKVR 12
DB 356 AKQNLNKVK 365

QY 2 FAWKRNMRKV 11
DB 42 FAWYRGLRKI 51

Search completed: February 21, 2003, 08:00:47
Job time : 22.6744 secs

RESULT 14
Q9POS6
ID Q9POS6 PRELIMINARY; PRT; 386 AA.
AC Q9POS6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Serine/threonine kinase.
GN PKN OR UU216.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=SEROVAR 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
urealyticum.";
RL Nature 407:757-762(2000).
DR EMBL; AB002120; AAF30624.1; -;
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN 1.
KW ATP-binding; Transferase; Complete proteome.
SQ SEQUENCE 386 AA; 45241 MW; 789374CC15D1CAD9 CRC64;

Query Match 57.1%; Score 40; DB 16; Length 386;
Best Local Similarity 54.5%; Pred.No. 39; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 2;

QY 1 CFAWKNMRKV 11
DB 290 CFAWKEDNKL 300

RESULT 15
Q63104
ID Q63104 PRELIMINARY; PRT; 114 AA.
AC Q63104;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-JAN-1999 (TReMBLrel. 09, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Carcinoembryonic antigen (fragment).
GN CEA4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=BD II; TISSUE=LIVER;
RX MEDLINE=89214106; PubMed=2708349;
RA Kodelja V., Lucas K., Barnert S., von Kleist S., Thompson J.A.,
RA Zimmermann W.A.;
RT "Identification of a carcinoembryonic antigen gene family in the rat:
Analysis of the N-terminal domains reveals immunoglobulin-like,
hypervariable regions.";
RL J. Biol. Chem. 264:6906-6912(1989).
DR EMBL; M60026; AAA40911.1; -;
FT NON TER 1
SQ SEQUENCE 114 AA; 12832 MW; 3AE108689B061686 CRC64;

Query Match 55.7%; Score 39; DB 11; Length 114;
Best Local Similarity 50.0%; Pred.No. 17; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:37:21 ; Search time 28.093 Seconds
(without alignments)
56.918 Million cell updates/sec

Title: US-09-743-107B-95
Perfect score: 58
Sequence: 1 CFAWQRAVRKVR 12

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	12	21	AA198095
2	63	92.6	12	21	AA198074
3	62	91.2	12	21	AA198070
4	59	86.8	12	21	AA198089
5	59	86.8	12	21	AA198090
6	59	86.8	12	21	AA198093
7	58	85.3	12	21	AA198086
8	58	85.3	12	21	AA198094
9	57	83.8	12	21	AA198038
10	57	83.8	12	21	AA198046

11	57	83.8	12	21	AA198047	Human lactoferrin
12	57	83.8	13	21	AA198037	Human lactoferrin
13	57	83.8	13	21	AA198048	Human lactoferrin
14	57	83.8	13	21	AA198049	Human lactoferrin
15	57	83.8	14	21	AA198036	Human lactoferrin
16	57	83.8	14	21	AA198050	Human lactoferrin
17	57	83.8	14	21	AA198051	Human lactoferrin
18	57	83.8	15	17	AA198554	Peptide for anti-u
19	57	83.8	15	21	AA198035	Human lactoferrin
20	57	83.8	15	21	AA198062	Human lactoferrin
21	57	83.8	15	21	AA198063	Human lactoferrin
22	57	83.8	16	21	AA198031	Human lactoferrin
23	57	83.8	16	21	AA198064	Human lactoferrin
24	57	83.8	16	21	AA198065	Human lactoferrin
25	57	83.8	17	21	AA198034	Human lactoferrin
26	57	83.8	17	21	AA198066	Human lactoferrin
27	57	83.8	17	21	AA198067	Human lactoferrin
28	57	83.8	18	15	AA198352	Human lactoferrin
29	57	83.8	18	17	AA198397	Advanced glycosyla
30	57	83.8	18	21	AA198033	Human lactoferrin
31	57	83.8	19	21	AA198867	Amino acid sequenc
32	57	83.8	19	21	AA198032	Human lactoferrin
33	57	83.8	20	13	AA1981810	Anti microbial pep
34	57	83.8	20	14	AA1984841	Lactoferrin-relate
35	57	83.8	20	15	AA198530	Lactoferrin derive
36	57	83.8	20	15	AA198531	Lactoferrin derive
37	57	83.8	20	15	AA1987461	Lactoferrin derive
38	57	83.8	20	15	AA1987462	Lactoferrin derive
39	57	83.8	20	16	AA1984698	Bovine lactoferrin
40	57	83.8	20	16	AA1984699	Bovine lactoferrin
41	57	83.8	20	16	AA1980263	Anti-parasitic lac
42	57	83.8	20	16	AA1980264	Anti-parasitic lac
43	57	83.8	20	17	AA1988553	Peptide for anti-u
44	57	83.8	20	17	AA1981852	Lactoferrin-derive
45	57	83.8	20	17	AA1980345	Lactoferrin-derive

ALIGNMENTS

RESULT 1

AA198095
ID AA198095 standard; Peptide; 12 AA.
XX AA198095;
AC AA198095;
XX AA198095;
DT 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:95.

Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.

OS Homo sapiens.
OS Synthetic.

XX WO200001730-A1.

PD 13-JAN-2000.

XX 06-JUL-1999; 99WO-S001230.

PR 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 38; 102pp; English.
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX Sequence 12 AA;
SQ Query Match 100.0%; Score 68; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFAWQRAWRKVR 12
DB |||||
1 CFAWQRAWRKVR 12
RESULT 2
AAY78074
ID AAY78074 standard; Peptide; 12 AA.
AC AAY78074;
XX 25-APR-2000 (first entry)
DT Human lactoferrin derived peptide SEQ ID NO:74.
DE Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
PN 13-JAN-2000.
PD 06-JUL-1999; 99WO-SE01230.
PF 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI WPI; 2000-147388/13.
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 35; 102pp; English.
XX AAY78001 to AAY78100 represent peptides having sequences based on human

CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX Sequence 12 AA;
SQ Query Match 92.6%; Score 63; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00038;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFAWQRAWRKVR 12
DB |||||
1 CFAWQRAWRKVR 12
RESULT 3
AAY78070
ID AAY78070 standard; Peptide; 12 AA.
AC AAY78070;
XX 25-APR-2000 (first entry)
DT Human lactoferrin derived peptide SEQ ID NO:70.
DE Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.
XX Homo sapiens.
OS Synthetic.
XX WO200001730-A1.
PN 13-JAN-2000.
PD 06-JUL-1999; 99WO-SE01230.
PF 06-JUL-1998; 98SE-0002441.
PR 17-JUL-1998; 98SE-0002562.
PR 29-DEC-1998; 98SE-0004614.
XX (ASCI-) A+ SCI INVEST AB.
PA Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
PI WPI; 2000-147388/13.
XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX Claim 22; Page 35; 102pp; English.
XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX Sequence 12 AA;

SQ Query Match 91.2%; Score 62; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00057;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAMQRMKVR 12
 |||||
 Db 1 CFAMQRMKVR 12

RESULT 4

AAV78089
 ID AAY78089 standard; Peptide; 12 AA.

XX AC AAY78089;

XX DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:89.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.

OS Synthetic.

XX FN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT Claim 22; Page 37; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 86.8%; Score 59; DB 21; Length 12;
 Best Local Similarity 83.3%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAMQRMKVR 12
 |||||
 Db 1 CFAMQRMKVR 12

RESULT 5

AAV78090
 ID AAY78090 standard; Peptide; 12 AA.

XX AC AAY78090;

XX DT 25-APR-2000 (first entry)

DE Human lactoferrin derived peptide SEQ ID NO:90.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT Claim 22; Page 37; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 86.8%; Score 59; DB 21; Length 12;
 Best Local Similarity 83.3%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRAWKVR 12
 DB 1 CFQWQRAWKVR 12

RESULT 6

AAV78093
 ID AAV78093 standard; Peptide; 12 AA.

XX AC AAY78093;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:93.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

OS Homo sapiens.
 OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 22; Page 38; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 86.8%; Score 59; DB 21; Length 12;

Best Local Similarity 83.3%; Pred. No. 0.0018;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFAWQRAWKVR 12

DB 1 CFQWQRAWKVR 12

RESULT 7

AAV78086

ID AAY78086 standard; Peptide; 12 AA.

XX AC AAY78086;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:86.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

OS Homo sapiens.
 OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,
 XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 22; Page 36; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 85.3%; Score 58; DB 21; Length 12;

Best Local Similarity 83.3%; Pred. No. 0.0027;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRAWKVR 12

DB 1 CFQWQRAWKVR 12

RESULT 8

AAV78094

ID AAY78094 standard; Peptide; 12 AA.

XX AC AAY78094;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:94.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SE01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Matesby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 22; Page 38; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 12 AA;
 Query Match 85.3%; Score 58; DB 21; Length 12;
 Best Local Similarity 83.3%; Pred. No. 0.0027;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFAMQRAMRKVR 12
 |||||
 DB 1 CFAMQNNRKVR 12
 |||||
 RESULT 9
 AAY78038
 ID AAY78038 standard; Peptide; 12 AA.
 XX
 AC AAY78038;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:38.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.

OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SE01230.
 XX
 PR 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 PA (ASCI-) A+ SCI INVEST AB.
 XX
 PI Hanson LA, Matesby-Baltzer I, Baltzer L, Dolphin GT;
 XX
 DR WPI; 2000-147388/13.
 XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 XX
 PS Claim 12; Page 70; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 SQ Sequence 12 AA;
 Query Match 83.8%; Score 57; DB 21; Length 12;
 Best Local Similarity 83.3%; Pred. No. 0.0039;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CFAMQRAMRKVR 12
 |||||
 DB 1 CFAMQNNRKVR 12
 |||||
 RESULT 10
 AAY78046
 ID AAY78046 standard; Peptide; 12 AA.
 XX
 AC AAY78046;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human lactoferrin derived peptide SEQ ID NO:46.
 XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 35; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 83.8%; Score 57; DB 21; Length 12;
 Best Local Similarity 83.3%; Pred. No. 0.0039;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12
 Db |||||
 1 CFQWQRNMRKVR 12

RESULT 11

AAV78047
 ID AAY78047 standard; Peptide; 12 AA.

AC AAY78047;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:47.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 35; 102pp; English.

PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX WPI; 2000-147388/13.
 DR New peptides used for treatment and prevention of infections,
 XX inflammations and tumors and for use in infant formula food -
 PT Claim 18; Page 73; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 83.8%; Score 57; DB 21; Length 12;
 Best Local Similarity 83.3%; Pred. No. 0.0039;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRNMRKVR 12
 Db |||||
 1 CFQWQRNMRKVR 12

RESULT 12

AAV78037
 ID AAY78037 standard; Peptide; 13 AA.

XX AAY78037;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX Homo sapiens.
 OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX Claim 18; Page 73; 102pp; English.

CC RAY78001 to RAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medical product of the peptide or fragment
CC can be used for treating and/or prevention of infections such as

CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;

Query Match 83.8%; Score 57; DB 21; Length 13;

Best Local Similarity 83.3%; Pred. No. 0.0042;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQAMRKVR 12

Db 2 CFQWRNRKVR 13

RESULT 15

AAAY78036

ID AAY78036 standard; Peptide; 14 AA.

XX AC AAY78036;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:36.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;

XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

XX KW urinary tract infection; colitis; Candida infection; fungicidal;

XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, MattsBy-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food

XX PS Claim 12; Page 69; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human

XX CC lactoferrin. The peptides are taken up in the intestine through

XX CC binding to specific lactoferrin receptors and are then transported

XX CC through the circulation. A medicinal product of the peptide or fragment

XX CC can be used for treating and/or prevention of infections (such as

XX CC urinary tract infections, colitis, and candida infection on a mucosal

XX CC membrane), inflammations and/or tumours. The peptides can also be used

XX CC in food stuffs such as infant formula food. The peptides are also

XX CC fungicidal and bactericidal and may also be used as preservatives.

XX CC Even though native human lactoferrin have been shown to have desired

XX CC anti-inflammatory anti-infectious and anti-tumoural properties they

XX CC cannot be used clinically on a broad basis because of high production

XX CC costs. Therefore, provision of peptides based on lactoferrin would

XX CC enable them to be used for the same purposes as lactoferrin at lower

XX CC cost.

XX SQ Sequence 14 AA;

Query Match 83.8%; Score 57; DB 21; Length 14;

Best Local Similarity 83.3%; Pred. No. 0.0045;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQAMRKVR 12

Db 3 CFQWRNRKVR 14

Search completed: February 21, 2003, 07:56:45

Job time : 29.093 secs

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Run on: February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds
(without alignments)
39.537 Million cell updates/sec

Title: US-09-743-107b-95

Perfect score: 68

Sequence: 1 CFAWQRAVRKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	57	83.8	18	1	US-08-204-487-3
2	57	83.8	18	2	US-08-485-948-8
3	57	83.8	18	2	US-08-628-380-8
4	57	83.8	18	2	US-08-475-055-8
5	57	83.8	20	1	US-07-755-161A-3
6	57	83.8	20	1	US-07-891-174-3
7	57	83.8	20	1	US-08-204-487-1
8	57	83.8	20	1	US-08-256-771-24
9	57	83.8	20	1	US-08-256-771-25
10	57	83.8	20	1	US-08-381-984-24
11	57	83.8	20	1	US-08-381-984-25
12	57	83.8	22	4	US-09-508-734-4
13	57	83.8	24	4	US-09-508-734-6
14	57	83.8	25	1	US-07-755-161A-10
15	57	83.8	25	1	US-07-891-174-10
16	57	83.8	25	1	US-08-204-487-7
17	57	83.8	29	4	US-09-508-734-8
18	57	83.8	36	1	US-07-755-161A-8
19	57	83.8	36	1	US-07-891-174-8
20	57	83.8	36	1	US-08-256-771-30
21	57	83.8	36	1	US-08-381-984-29
22	57	83.8	47	2	US-08-464-182A-6
23	57	83.8	47	2	US-08-406-271-6
24	57	83.8	50	2	US-08-693-274A-7
25	57	83.8	52	4	US-09-017-043A-3
26	57	83.8	53	2	US-08-464-182A-5
27	57	83.8	53	2	US-08-406-271-5

28	57	83.8	54	2	US-08-464-182A-2	Sequence 2, Appli
29	57	83.8	54	2	US-08-406-271-2	Sequence 2, Appli
30	57	83.8	694	3	US-08-724-586-2	Sequence 2, Appli
31	57	83.8	694	4	US-09-421-632-2	Sequence 2, Appli
32	57	83.8	694	4	US-09-932-190-2	Sequence 2, Appli
33	57	83.8	705	2	US-08-655-640-2	Sequence 2, Appli
34	57	83.8	708	2	US-08-655-640-4	Sequence 4, Appli
35	57	83.8	711	1	US-08-154-019-4	Sequence 4, Appli
36	57	83.8	711	1	US-08-461-333-4	Sequence 4, Appli
37	57	83.8	711	3	US-08-464-167-4	Sequence 4, Appli
38	57	83.8	711	3	US-09-158-313-4	Sequence 4, Appli
39	57	83.8	711	4	US-08-476-798-4	Sequence 4, Appli
40	54	79.4	711	1	US-08-145-681-2	Sequence 2, Appli
41	54	79.4	711	1	US-08-250-308-2	Sequence 2, Appli
42	54	79.4	711	1	US-08-453-703-2	Sequence 2, Appli
43	54	79.4	711	2	US-08-456-106-2	Sequence 2, Appli
44	54	79.4	711	3	US-08-456-108-2	Sequence 2, Appli
45	54	79.4	711	4	US-09-265-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37) "
US-08-204-487-3

Query Match 83.8%; Score 57; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQAMRKVR 12
||| ||| ||| |||
Db 1 CFQWQNMKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VIASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,948
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,217
; FILING DATE: JUNE 7, 1995
; APPLICATION NUMBER: 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-Cl, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-485-948-8

Query Match 83.8%; Score 57; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQAMRKVR 12
||| ||| ||| |||
Db 1 CFQWQNMKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VIASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,380
; FILING DATE: April 4, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,642
; FILING DATE: APRIL 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 947-1-008 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: LF-Cl, 8-25
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-628-380-8

Query Match 83.8%; Score 57; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQAMRKVR 12
||| ||| ||| |||
Db 1 CFQWQNMKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VIASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-Cl, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match      83.8%; Score 57; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWRMRKVR 12
Db 1 CFQWRMRKVR 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible

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OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

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Query Match

83.8%; Score 57; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 0.0017; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFAMQRMKVR 12
Db 2 CFQWQRMKVR 13

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 83.8%; Score 57; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0017; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFAMQRMKVR 12
Db 2 CFQWQRMKVR 13

RESULT 7
US-08-204-487-1
Sequence 1, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGEKI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBBAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000

Best Local Similarity 83.3%; Pred. No. 0.0017; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFAMQRMKVR 12
Db 2 CFQWQRMKVR 13

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 83.8%; Score 57; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0017; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFAMQRMKVR 12
Db 2 CFQWQRMKVR 13

RESULT 6
US-07-891-174-3
Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site

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TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..20
; OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
; OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 83.8%; Score 57; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0017; 2; Indels 0;
Matches 10; Conservative 0; Mismatches 2; Gaps 0;

QY 1 CFAWQAMRKVR 12
Db 2 CFQWQNMKVR 13

RESULT 8
US-08-256-771-24
; Sequence 24, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; PRODUCT'S THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are linked by
; OTHER INFORMATION: disulfide bond"
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US-08-256-771-24

Query Match 83.8%; Score 57; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0017; 2; Indels 0;
Matches 10; Conservative 0; Mismatches 2; Gaps 0;

QY 1 CFAWQAMRKVR 12
Db 2 CFQWQNMKVR 13

RESULT 9
US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; PRODUCT'S THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys residues are protected to
; OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25

Query Match 83.8%; Score 57; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0017; 2; Indels 0;
Matches 10; Conservative 0; Mismatches 2; Gaps 0;

QY 1 CFAWQAMRKVR 12
Db 2 CFQWQNMKVR 13

RESULT 10
US-08-381-984-24
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Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSES: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-24

Query Match 83.8%; Score 57; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRMKVR 12
DB 2 CFQWQRMKVR 13

RESULT 11
US-08-381-984-25
Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSES: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-25

Query Match 83.8%; Score 57; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRMKVR 12
DB 2 CFQWQRMKVR 13

RESULT 12
US-09-508-734-4
Sequence 4, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast an
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4

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; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4
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  Best Local Similarity 83.3%; Pred. No. 0.0019; 2; Indels 0; Gaps 0;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQRMNRKVR 12
Db 2 CFQWQRMNRKVR 13

RESULT 13
US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Sanyang Genex Corporation
; TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
; FILE REFERENCE: PA/SYG/00139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6

Query Match      83.8%; Score 57; DB 4; Length 24;
Best Local Similarity 83.3%; Pred. No. 0.002; 2; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQRMNRKVR 12
Db 3 CFQWQRMNRKVR 14

RESULT 14
US-07-755-161A-10
; Sequence 10, Application US/07755161A
; Patent No. 5304633
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,161A
; FILING DATE: 19910905
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURES:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURES:
; NAME/KEY: modified site
; LOCATION: 21
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10

Query Match      83.8%; Score 57; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CFQWQRMNRKVR 12
Db 4 CFQWQRMNRKVR 15
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RESULT 15
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
Query Match 83.8%; Score 57; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFAMQAMRKVR 12
Db 4 CFQMQRNKRVR 15
Search completed: February 21, 2003, 08:04:27
Job time : 8.93023 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 08:08:15 ; Search time 6.89372 Seconds
(without alignments)
54.162 Million cell updates/sec

Title: US-09-743-107b-95
Perfect score: 68
Sequence: 1 CFAMORAMEKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	83.8	15	9	US-09-798-869-2
2	57	83.8	25	9	US-09-798-869-20
3	57	83.8	694	9	US-10-023-096-2
4	49	72.1	15	9	US-09-798-869-6
5	47	69.1	15	9	US-09-798-869-3
6	47	69.1	25	9	US-09-798-869-23
7	42	61.8	15	9	US-09-798-869-4
8	42	61.8	25	9	US-09-798-869-22
9	39	57.4	15	9	US-09-798-869-7
10	39	57.4	15	9	US-09-798-869-8
11	39	57.4	15	9	US-09-798-869-29
12	39	57.4	15	9	US-09-798-869-30
13	38	55.9	138	9	US-10-013-379-14
14	27	54.4	2273	10	US-09-995-542-12
15	37	54.4	2310	10	US-09-995-542-10
16	36	52.9	210	9	US-09-738-626-4884
17	36	52.9	301	9	US-10-080-960-11
18	36	52.9	302	10	US-09-948-078-2
19	35	51.5	489	9	US-09-888-320-2

34 50.0 46 10 US-09-864-761-35744 Sequence 35744, A
34 50.0 69 10 US-09-804-969-17 Sequence 17, Appl
34 50.0 209 10 US-09-904-536-8 Sequence 8, Appl
34 50.0 209 10 US-09-904-536-9 Sequence 9, Appl
34 50.0 209 10 US-09-904-536-11 Sequence 11, Appl
34 50.0 209 10 US-09-904-536-12 Sequence 12, Appl
34 50.0 209 10 US-09-904-536-13 Sequence 13, Appl
34 50.0 209 10 US-09-904-536-14 Sequence 14, Appl
34 50.0 209 10 US-09-904-536-15 Sequence 15, Appl
34 50.0 209 10 US-09-904-536-16 Sequence 16, Appl
34 50.0 209 10 US-09-904-536-17 Sequence 17, Appl
34 50.0 209 10 US-09-904-536-18 Sequence 18, Appl
34 50.0 212 10 US-09-904-536-10 Sequence 10, Appl
34 50.0 235 9 US-10-095-449-6 Sequence 6, Appl
34 50.0 235 10 US-09-448-378-1 Sequence 1, Appl
34 50.0 235 10 US-09-983-806-6 Sequence 6, Appl
34 50.0 235 10 US-09-904-536-1 Sequence 1, Appl
34 50.0 365 9 US-10-109-533A-2 Sequence 2, Appl
34 50.0 372 9 US-09-764-868-1044 Sequence 1044, Ap
34 50.0 1192 9 US-10-170-102-2 Sequence 2, Appl
34 50.0 67 9 US-09-796-692-1487 Sequence 1487, Ap
34 48.5 81 10 US-09-864-761-41887 Sequence 41887, A
34 48.5 171 10 US-09-764-864-1119 Sequence 1119, Ap
34 48.5 171 10 US-09-764-864-1536 Sequence 1536, Ap
34 48.5 579 10 US-09-824-588-2 Sequence 2, Appl
34 48.5 620 10 US-09-764-864-1116 Sequence 1116, Ap

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication NO. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LAERS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2

Query Match 83.8%; Score 57; DB 9; Length 15;
Best Local Similarity 83.3%; Pred.No. 0.00055;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAMORAMEKVR 12
DB 3 CFQWQNMKVR 14

RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication NO. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON

APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match 83.8%; Score 57; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
||| |||||
Db 3 CFQWQRMKVR 14

RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; TITLE OF INVENTION: Lactoferrin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-8350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-023-096-2

Query Match 83.8%; Score 57; DB 9; Length 694;
Best Local Similarity 83.3%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
||| |||||
Db 22 CFQWQRMKVR 33

RESULT 4
US-09-798-869-6
; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (VSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match 72.1%; Score 49; DB 9; Length 15;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
||| |||||
Db 3 CFQWQRMKVR 14

RESULT 5
US-09-798-869-3
; Sequence 3, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (VSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-3

Query Match 69.1%; Score 47; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.029;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQARMKRV 11
|:|||||:
Db 3 CYQWQRMKRL 13

RESULT 6

US-09-798-869-23
; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23

Query Match 69.1%; Score 47; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.049;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQARMKRV 11
|:|||||:
Db 3 CYQWQRMKRL 13

RESULT 7

US-09-798-869-4
; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4

Query Match 61.8%; Score 42; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQARMKRV 11
|:|||||:
Db 3 CLRQWNEKRV 13

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQARMKRV 11
|:|||||:
Db 3 CYQWQRMKRL 13

RESULT 8

US-09-798-869-22
; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22

Query Match 61.8%; Score 42; DB 9; Length 25;
Best Local Similarity 63.6%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQARMKRV 11
|:|||||:
Db 3 CLRQWNEKRV 13

RESULT 9

US-09-798-869-7
; Sequence 7, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (modified form of homo sapiens
; OTHER INFORMATION: sequence)
US-09-798-869-7

Query Match 57.4%; Score 39; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.69;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQARMKRV 11
|:|||||:
Db 3 CYQWQRMKRL 13


```
RESULT 10
US-09-798-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
; OTHER INFORMATION: sequence)
US-09-798-869-8

Query Match          57.4%; Score 39; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.69;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQAMRKV 11
DB 3 CLRQWQRMKKL 13

RESULT 11
US-09-798-869-29
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29

Query Match          57.4%; Score 39; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.69;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQAMRKV 11
DB 3 CLRQWQRMKKL 13

RESULT 12
US-09-798-869-30
; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-30

Query Match          57.4%; Score 39; DB 9; Length 15;
Best Local Similarity 54.5%; Pred. No. 0.69;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQAMRKV 11
DB 3 CLRQWQRMKKL 13

RESULT 13
US-10-013-379-14
; Sequence 14, Application US/10013379
; Publication No. US20020188108A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Cate, Jamie H.
; APPLICANT: No. US20020188108A1, Harry F.
; APPLICANT: Yusupov, Marat M.
; APPLICANT: Yusupova, Guinara ZH
; APPLICANT: Baucum, Albion
; APPLICANT: Lancaster, Laura
; APPLICANT: Dallas, Anne
; TITLE OF INVENTION: X-RAY CRYSTAL STRUCTURES OF FUNCTIONAL
; COMPLEXES OF THE BACTERIAL RIBOSOME CONTAINING TRANSFER RNA
; TITLE OF INVENTION: AND MODEL MESSENGER RNAs
; FILE REFERENCE: 19629-7010
; CURRENT APPLICATION NUMBER: US/10/013,379
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: US 60/254,603
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: US 60/278,013
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/294,394
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Thermus thermophilus
; FEATURE:
; OTHER INFORMATION: 50S ribosomal protein L16
; OTHER INFORMATION: 16iyp
US-10-013-379-14

Query Match          55.9%; Score 38; DB 9; Length 138;
Best Local Similarity 70.0%; Pred. No. 9.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQAMRKV 11
```

db 115 FAWRAYMKV 124
|||||

RESULT 14

JS-09-995-542-12
; Sequence 12, Application US/09995542
; Patent No. US20020127647A1
; GENERAL INFORMATION:
; APPLICANT: Shutter, John
; APPLICANT: Ullias, Learni
; TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-658-A
; CURRENT APPLICATION NUMBER: US/09/995,542
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/253,520
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: Homo sapiens
JS-09-995-542-12

Query Match 54.4%; Score 37; DB 10; Length 2273;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2Y 1 CFAWQRAM 8

db 779 CFAWQDRM 786
|||||

RESULT 15

JS-09-995-542-10
; Sequence 10, Application US/09995542
; Patent No. US20020127647A1
; GENERAL INFORMATION:
; APPLICANT: Shutter, John
; APPLICANT: Ullias, Learni
; TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-658-A
; CURRENT APPLICATION NUMBER: US/09/995,542
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/253,520
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 2310
; TYPE: PRT
; ORGANISM: Mus musculus
JS-09-995-542-10

Query Match 54.4%; Score 37; DB 10; Length 2310;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2Y 1 CFAWQRAM 8

db 779 CFAWQDRM 786
|||||

Search completed: February 21, 2003, 08:11:58
Job time : 7.88372 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:48:01 ; Search time 10.6047 Seconds
(without alignments)
108.784 Million cell updates/sec

Title: US-09-743-107b-95

Perfect score: 68

Sequence: 1 CFAWQSAWKVR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR73:**

1: PIR1:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	57	83.8	711	1	TFHUL	lactotransferrin p
2	47	69.1	708	2	JC2323	lactoferrin - goat
3	44	64.7	33	2	SS2107	lactoferrin - shee
4	43	63.2	500	2	G71633	ADP,ATP carrier pr
5	42	61.8	121	2	AH3147	hypothetical prote
6	42	61.8	707	1	A28438	lactoferrin precu
7	40	58.8	114	2	D33876	carcinoembryonic a
8	40	58.8	306	1	A39654	cell cycle arrest
9	39	57.4	511	2	AB0858	hypothetical prote
10	39	57.4	1135	2	T14803	phytochrome C - so
11	38	55.9	289	2	G86403	33.3K hypothetica
12	38	55.9	561	2	B82395	methy1-accepting c
13	37	54.4	161	2	AC3242	NTP pyrophosphohy
14	37	54.4	202	2	C71306	hypothetical prote
15	37	54.4	206	2	H97451	pyridoxamine 5'-ph
16	37	54.4	206	2	AB2670	pyridoxamine 5'-ph
17	37	54.4	208	2	AC3441	Probable pyridoxam
18	37	54.4	275	1	JCL113	interleukin-2 rece
19	37	54.4	275	1	S07442	interleukin-2 rece
20	37	54.4	294	2	T00104	probable drpp-4-de
21	37	54.4	303	1	WZBEM6	gene 20 protein -
22	37	54.4	303	2	C33374	hypothetical prote
23	37	54.4	337	2	B97374	Dainococcus radiod
24	37	54.4	337	2	AH2591	membrane lipoprote
25	37	54.4	494	2	F83199	Probable carbonydr
26	37	54.4	499	2	B97842	ADP,ATP carrier pr
27	37	54.4	502	2	T01179	hypothetical prote
28	37	54.4	584	2	C94325	hypothetical prote
29	37	54.4	601	2	JE0238	stress protein p66

30 37 54.4 1636 2 B82736 hemolysin-type cal
31 37 54.4 2700 2 D88450 protein F21H11.2 [
32 37 54.4 4568 2 T08030 dynein beta heavy
33 36.5 53.7 278 2 AD0651 probable membrane
34 36 52.9 396 2 E90238 threonine synthase
35 36 52.9 456 2 C86624 hypothetical prote
36 36 52.9 456 2 H72000 hypothetical prote
37 36 52.9 541 2 C81357 probable secreted
38 36 52.9 807 1 WWAD15 late 100K protein
39 36 52.9 956 2 B71250 valine-tRNA ligase
40 36 52.9 1081 2 T31329 receptor tyrosine
41 36 52.9 1165 2 D59433 C. elegans protein
42 36 52.9 1746 2 D83191 hypothetical prote
43 35 51.5 228 2 AS0438 conserved hypotet
44 35 51.5 243 2 S25308 probable phycocyan
45 35 51.5 275 2 T22597 hypothetical prote

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61189; A31000; S7
R/Cho, Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237

R/Key, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A/Cross-references: EMBL:X53961; NID:g34415; PIDN:CAA37914.1; PID:g34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactofe

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312

A/Experimental source: placenta

A/Notes: sequence extracted from NCBI backbone (NCBI:P:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <STI>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>

```
F:359-696/Domain: transferin repeat homology <1kHz>
F:252,300,387,495,564/Binding site: carbohydrate (Asn)
#status predicted (covalent)
```

J. Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Rao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AH3147
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-121 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AAU45598.1; PID:gl7743317; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu4804
 A:Map position: linear chromosome

Query Match 61.8%; Score 42; DB 2; Length 121;
 Best Local Similarity 63.6%; Pred. No. 2.2;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQARMKV 11
 |||||
 Db 14 CLAWQRRRV 24

RESULT 6

A28438
 lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 R:Accession: A28438; A1205
 R:Protein: B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretory granules
 A:Reference number: A92596; MUID:87280033; PMID:3611056
 A:Accession: A28438
 A:Molecule type: mRNA
 A:Residues: 3-707 <PEN>
 A:Cross-references: EMBL:J03298
 R:Li, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A>Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A:Reference number: A1205; MUID:92042099; PMID:1939212
 A:Accession: A1205
 A:Molecule type: DNA
 A:Residues: 1-15 <LIU>
 A:Cross-references: GB:M74778
 C:Superfamily: transferrin; transferrin repeat homology
 F:1-19/Domain: duplication; glycoprotein
 F:20-707/Product: signal sequence #status predicted <SIG>
 F:358-695/Domain: transferrin repeat homology <TRH2>
 F:194/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.8%; Score 42; DB 1; Length 707;
 Best Local Similarity 63.6%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQARMKV 11
 |||||
 Db 37 CLRWQNRKV 47

RESULT 7

D33876
 carcinoembryonic antigen homolog 4 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jul-1999
 C:Accession: D33876
 R:Kodelja, V.; Lucas, K.; Barnert, S.; von Kleist, S.; Thompson, J.A.; Zimmermann, W.
 J. Biol. Chem. 264, 6906-6912, 1989
 A>Title: Identification of a carcinoembryonic antigen gene family in the rat. Analysis of

A:Reference number: A33876; MUID:89214106; PMID:2708349
 A:Accession: D33876
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-114 <KOD>
 A:Cross-references: GB:M60026; NID:G203407; PIDN:AAA40911.1; PID:G554427; GB:J04626; C
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic precursor amino-term

Query Match 58.8%; Score 40; DB 2; Length 114;
 Best Local Similarity 60.0%; Pred. No. 4.8;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQARMKV 11
 |||||
 Db 42 FAWYGLRKI 51

RESULT 8

A39654
 cell cycle arrest protein BUB2 - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YMR9796.08c; protein YMR055c
 C:Species: Saccharomyces cerevisiae
 C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jul-2000
 C:Accession: A39654; S5455; S19034
 R:Hoyt, M.A.; Totis, L.; Roberts, B.T.
 Cell 66, 507-517, 1991
 A>Title: Saccharomyces cerevisiae genes required for cell cycle arrest in response to
 A:Reference number: A39654; MUID:91330299; PMID:1651171
 A:Accession: A39654
 A:Molecule type: DNA
 A:Residues: 1-306 <HOY>
 A:Cross-references: GB:M64706; NID:gl71133; PIDN:AAA16885.1; PID:gl71135
 R:Devlin, K.; Churcher, C.M.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54548
 A:Accession: S5455
 A:Molecule type: DNA
 A:Residues: 1-306 <DEV>
 A:Cross-references: EMBL:Z49703; NID:gl71880; PIDN:CAA89765.1; PID:gl71888; GSPDB:GN00

Query Match 58.8%; Score 40; DB 1; Length 306;
 Best Local Similarity 60.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQARMKV 10
 |||||
 Db 108 CFAWQTOQR 117

RESULT 9

AB0858
 hypothetical protein STV3070 [imported] - Salmonella enterica subsp. enterica serovar
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A>Note: this species has also been called Salmonella typhi
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AB0858
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra
 , S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K
 A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser.
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AB0858
 A>Status: preliminary
 A:Molecule type: DNA

QY 1 CFAWQAMRKVR 12
|||:
Db 8 CFTWEYARHVR 19

RESULT 12
E82395 methyl-accepting chemotaxis protein VCA0974 [imported] - Vibrio cholerae (strain N169)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82395
R;Reidberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Drygoid, I.; Sellers
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 408, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; UID:20406833; PMID:10952301
A;Accession: E82395
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-561 <HEI>
A;Cross-references: GB:AE004423; GB:AE003853; NID:g9658400; PIDN:AAF96870.1; GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0974
A;Map position: 2

Query Match 55.9%; Score 38; DB 2; Length 561;
Best Local Similarity 63.6%; Pred. NO. 51;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FAWQAMRKVR 12
|||:
Db 7 FAWQALRLKR 17

RESULT 13
AC3242 NTP pyrophosphohydrolase, MutT family [imported] - Agrobacterium tumefaciens (strain
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AC3242
R;Wood, D.W.; Sebubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl
l; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, S.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AC3242
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-161 <KUR>
A;Cross-references: GB:AE008650; PIDN:RAL46353.1; PID:gl7744142; GSPDB:GNC0189
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: tiorf74
A;Genome: plasmid

Query Match 54.4%; Score 37; DB 2; Length 161;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 AWQAMRKVR 12
|||:
Db 51 AWEALREVR 60

RESULT 14
C71306
hypotheoretical protein TP0594 - syphilis spirochete
C-Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
 C/Accession: C71306
 R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A>Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
 A/Reference number: A71250; MUID:9832770; PMID:9665876
 A/Accession: C71306
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-202 <COL>
 A/Cross-references: GB:AE001234; GB:AE000520; NID:g3322881; PIDN:AAC65572.1; PID:g332289
 A/Experimental source: strain Nichols
 C/Genetics:
 A/Gene: TP0594

Query Match 54.4%; Score 37; DB 2; Length 202;
 Best Local Similarity 87.5%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 WQAMRKV 11
 DB 21 WQAMRKV 28

RESULT 15

H97451
 Pyridoxamine 5'-phosphate oxidase (A179611) [imported] - *Agrobacterium tumefaciens* (str
 C/Species: *Agrobacterium tumefaciens*
 C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C/Accession: H97451
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
 Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
 A/Reference number: A97359; PMID:11743194
 A/Accession: H97451
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-206 <KUR>
 A/Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169
 C/Genetics:
 A/Gene: AGR_C_1381
 A/Map position: circular chromosome
 C/Superfamily: pyridoxamine-phosphate oxidase

Query Match 54.4%; Score 37; DB 2; Length 206;
 Best Local Similarity 50.0%; Pred. No. 29;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAMQAMRKVR 12
 DB 88 CFHWKSLRRQVR 99

Search completed: February 21, 2003, 08:02:49
 Job time : 11.6047 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:28:06 ; Search.time 5.2093 Seconds
(without alignments)
95.544 Million cell updates/sec

Title: US-09-743-107b-95

Perfect score: 68

Sequence: 1 CFANQAMRKVR 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	83.8	711	1 TRFL_HUMAN	P02788 homo sapien
2	47	69.1	708	1 TRFL_CAMDR	Q9tun0 camelus dro
3	47	69.1	708	1 TRFL_CAPHI	Q29477 capra hircu
4	43	63.2	500	1 TLCE_RICPR	O05962 rickettsia
5	42	61.8	707	1 TRFL_MOUSE	P08071 mus musculus
6	40	58.8	306	1 BUB2_YEAST	P26448 saccharomyc
7	39	57.4	1135	1 PHYC_SORBI	P93528 sorghum bic
8	37	54.4	275	1 IL2A_BOVIN	P12342 bos taurus
9	37	54.4	275	1 IL2A_SHEEP	P26898 ovina aries
10	37	54.4	303	1 UL24_HSVSA	Q01005 herpesvirus
11	37	54.4	601	1 WD66_PHYPO	P90587 physarum po
12	37	54.4	1137	1 PHYC_ORYSA	Q92w19 oryza sativ
13	37	54.4	1179	1 ATX1_ARATH	O91t02 arabidopsis
14	37	54.4	2273	1 ABCR_HUMAN	P78363 homo sapien
15	37	54.4	4568	1 DYHE_CHLRE	Q39865 chlamydomon
16	36	52.9	267	1 RS3A_DROME	P55830 drosophila
17	36	52.9	363	1 CTNS_DROME	Q9vcr7 drosophila
18	36	52.9	695	1 TRFL_HORSE	O77811 equus cabal
19	36	52.9	805	1 L100_ADR02	P24932 human adeno
20	36	52.9	807	1 L100_ADR05	P24933 human adeno
21	36	52.9	956	1 SVV_TFEPA	O83988 treponema p
22	36	52.9	1208	1 RCQJ_HUMAN	O94761 homo sapien
23	35	51.5	242	1 PYG_GALSU	Q02074 gaidieria s
24	35	51.5	275	1 VA16_VACCV	P16710 vaccinia vi
25	35	51.5	378	1 VA16_VACCC	P20993 vaccinia vi
26	35	51.5	538	1 R060_HUMAN	P10155 homo sapien
27	35	51.5	538	1 R060_MOUSE	O08848 mus musculus
28	35	51.5	538	1 R060_XENLA	P42700 xenopus lae
29	35	51.5	1214	1 TSGA_RAT	Q63679 rattus norv
30	35	51.5	1574	1 RPOC_AQUAE	O67763 aquifex aeo
31	35	51.5	1576	1 RPOC_AQUPY	Q9x6y2 aquifex pyr
32	34	50.0	85	1 PMRD_SALTY	P37589 salmonella
33	34	50.0	116	1 MERT_SALTI	P04336 salmonella

ALIGNMENTS

RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; Q16780; Q16785; Q16786; Q16789; Q00756; Q9H1Z3; Q96KZ4;			
AC	Q96KZ5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lactotransferrin precursor (Lactoferrin) (Contains: Lactoferrin A;			
DE	Lactoferrin B; Lactoferrin C).			
GN	LIF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RL	Nucleic Acids Res. 18:5288-5288(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RA	Cho Y.Y.;			
RL	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Connely O.M.;			
RL	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RL	"Molecular cloning and sequence analysis of human lactoferrin.";			
RN	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RL	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RT	sequences.";			
RL	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary Gland;			
RA	Cheng H., Chen X., Huan L.;			
RL	"cDNA cloning and sequence analysis of human lactoferrin.";			
RN	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			

O19999 cyanidium c
P49771 homo sapien
Q11059 mycobacteri
P21159 myxococcus
Q9CX47 mus musculu
P03502 influenza b
Q15743 homo sapien
P37143 methylobacti
Q82y48 pyrobaculum
Q41046 pinus sylve
Q24595 drosophila
Q50651 mycobacteri

PP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE-Mammary gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=9076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RA Legrand D., Spik G., Montreuil J., Jolles P.;
RT "Human lactoferrin: amino acid sequence and structural
comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RA Jolles P.;
RT "The present state of the human lactotransferrin sequence, study and
alignment of the cyanogen bromide fragments and characterization of
N- and C-terminal domains.";
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RA Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
lactotransferrin.";
RL FEBS Lett. 142:1107-110(1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Choj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RL [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human diferric lactoferrin refined at 2.2-A
resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
binding properties and crystal structure of the histidine-
253-->methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in *Aspergillus
awamori*.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
and analysis of ligand-induced conformational change.";
RL Acta Crystallogr. D 54:1319-1335(1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioid antagonist peptides derived
from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
RA El Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejtmancik J.F., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RL Mol. Vision 4:31-32(1998).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
CC -!- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC [14]
DR EMBL; X53961; CAA37914.1; -
DR EMBL; U07643; AAB60324.1; -
DR EMBL; M93150; AAA36159.1; -
DR EMBL; M83202; AAA59511.1; -
DR EMBL; M83205; AAA58656.1; -
DR EMBL; M18642; AAA86665.1; -
DR EMBL; AF332168; AAG48753.1; -
DR EMBL; SC015822; AAHL5822.1; -
DR EMBL; EC015823; AAHL5823.1; -
DR EMBL; M73700; AAA59479.1; -
DR EMBL; X52941; CAA37116.1; -
DR EMBL; U95626; AAB57795.1; -
DR PIR; S11228; TFHUL.
DR PDB; 1LCF; 31-AUG-94.
DR PDB; 1LCT; 31-OCT-93.
DR PDB; 1LFG; 31-JUL-94.
DR PDB; 1LFH; 31-OCT-93.
DR PDB; 1LFI; 31-OCT-93.
DR PDB; 1LGB; 31-AUG-94.
DR PDB; 1LGC; 31-AUG-94.
DR PDB; 1BKA; 08-NOV-96.
DR PDB; 1DSN; 08-MAR-96.
DR PDB; 1HSE; 12-MAR-97.
DR PDB; 1VFD; 21-APR-97.

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Query Match      83.8%; Score 57; DB 1; Length 711;
Best Local Similarity 83.3%; Pred. No. 0.0052;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
   |||||
Db 39 CFQWQRMKVR 50

RESULT 2
TRFL_CAMDR
ID TRFL CAMDR STANDARD; PRT; 708 AA.
AC Q9TUM0; Q9WZS5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin)
GN LTF.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sonali; TISSUE=Lactating mammary gland;
RA Kappeler S.R., Ackermann M., Farah Z., Puhon Z.;
RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
RL Int. Dairy J. 9:481-486(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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DR EMBL; AJ131674; CAB53387.1; -
DR EMBL; AF165879; AAF82241.1; -
DR HSSP; O77811; 1B1X.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SW000594; TR_FER_2
DR PROSITE; PS00205; TRANSFERRIN 1; 2.
DR PROSITE; PS00206; TRANSFERRIN 2; 2.
DR PROSITE; PS00207; TRANSFERRIN 3; 2.
DR Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal.
FT CHAIN 1 19 BY SIMILARITY.
FT CHAIN 20 708 LACTOTRANSFERRIN.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT DISULFID 28 64 BY SIMILARITY.
FT DISULFID 38 55 BY SIMILARITY.
FT DISULFID 134 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.

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FT DISULFID 377 390 BY SIMILARITY.
FT DISULFID 424 703 BY SIMILARITY.
FT DISULFID 444 666 BY SIMILARITY.
FT DISULFID 476 551 BY SIMILARITY.
FT DISULFID 500 694 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 IRON 1 (BY SIMILARITY).
FT METAL 111 IRON 1 (BY SIMILARITY).
FT METAL 211 211 IRON 1 (BY SIMILARITY).
FT METAL 272 272 IRON 1 (BY SIMILARITY).
FT METAL 414 414 IRON 2 (BY SIMILARITY).
FT METAL 452 452 IRON 2 (BY SIMILARITY).
FT METAL 545 545 IRON 2 (BY SIMILARITY).
FT METAL 614 614 IRON 2 (BY SIMILARITY).
FT BINDING 140 140 ANION (BY SIMILARITY).
FT BINDING 482 482 ANION (BY SIMILARITY).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 261 261 F -> S (IN REF. 2).
FT CONFLICT 304 304 G -> A (IN REF. 2).
FT CONFLICT 330 330 S -> P (IN REF. 2).
FT CONFLICT 492 494 LJS -> PLF (IN REF. 2).
FT CONFLICT 506 506 L -> F (IN REF. 2).
FT CONFLICT 609 609 A -> P (IN REF. 2).
FT CONFLICT 642 642 R -> Q (IN REF. 2).
SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;

Query Match      69.1%; Score 47; DB 1; Length 708;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQWQRMKVR 12
   |||||
Db 38 CAQWQRMKVR 49

RESULT 3
TRFL_CAPHI
ID TRFL_CAPHI STANDARD; PRT; 708 AA.
AC Q29477; Q29479;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (lactoferrin)
GN LTF.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Lee T., Yu S., Kim S., Lee K., Yu D.;
RA Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=94380047; PubMed=8093048;
RA le Provost F., Nocard M., Guerin G., Martin P.;
RT "Characterization of the goat lactoferrin cDNA. Assignment of the
RT relevant locus to bovine U12 syntenic group.";
RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC

```

CC -I- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -I- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; X53857; AAA97958.1; -;
 CC DR EMBL; X78902; CAA55517.1; -;
 CC DR HSSP; O77698; 1CE2.
 CC DR InterPro; IPR001156; Transferrin.
 CC DR Pfam; PF00405; transferrin; 2.
 CC DR PRINTS; PR00422; TRANSFERRIN.
 CC DR SMART; SMO0094; TFF; 2.
 CC DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 CC DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 CC DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 CC KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 CC Signal.
 CC FT CHAIN 1 19 BY SIMILARITY.
 CC FT REPEAT 20 708 LACTOTRANSFERRIN.
 CC FT REPEAT 364 708 1.
 CC FT DISULFID 28 64 BY SIMILARITY.
 CC FT DISULFID 38 55 BY SIMILARITY.
 CC FT DISULFID 134 217 BY SIMILARITY.
 CC FT DISULFID 176 192 BY SIMILARITY.
 CC FT DISULFID 189 200 BY SIMILARITY.
 CC FT DISULFID 250 264 BY SIMILARITY.
 CC FT DISULFID 367 399 BY SIMILARITY.
 CC FT DISULFID 377 390 BY SIMILARITY.
 CC FT DISULFID 424 703 BY SIMILARITY.
 CC FT DISULFID 444 666 BY SIMILARITY.
 CC FT DISULFID 476 551 BY SIMILARITY.
 CC FT DISULFID 500 694 BY SIMILARITY.
 CC FT DISULFID 510 524 BY SIMILARITY.
 CC FT DISULFID 521 534 BY SIMILARITY.
 CC FT DISULFID 592 606 BY SIMILARITY.
 CC FT DISULFID 644 649 BY SIMILARITY.
 CC FT METAL 79 79 IRON 1 (BY SIMILARITY).
 CC FT METAL 111 111 IRON 1 (BY SIMILARITY).
 CC FT METAL 211 211 IRON 1 (BY SIMILARITY).
 CC FT METAL 272 272 IRON 1 (BY SIMILARITY).
 CC FT METAL 414 414 IRON 2 (BY SIMILARITY).
 CC FT METAL 452 452 IRON 2 (BY SIMILARITY).
 CC FT METAL 545 545 IRON 2 (BY SIMILARITY).
 CC FT METAL 614 614 IRON 2 (BY SIMILARITY).
 CC FT BINDING 140 140 ANION (BY SIMILARITY).
 CC FT BINDING 482 482 ANION (BY SIMILARITY).
 CC FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CONFLICT 56 56 I -> V (IN REF. 2).
 CC FT CONFLICT 88 88 L -> R (IN REF. 2).
 CC FT CONFLICT 124 124 Q -> K (IN REF. 2).
 CC FT CONFLICT 154 154 F -> P (IN REF. 2).
 CC FT CONFLICT 304 304 S -> R (IN REF. 2).
 CC FT CONFLICT 414 414 D -> G (IN REF. 2).
 CC SQ SEQUENCE 708 AA; 77358 MW; F2EDA3C83539960D CRC64;

Query Match 69.1%; Score 47; DB 1; Length 708;
 Best Local Similarity 63.6%; Pred.No. 0.37;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 11
 : : : : :
 DB 38 CYQWRMRKL 48

RESULT 4
 TLCE_RICPR STANDARD; PRT; 500 AA.
 AC O05962;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP-ATP carrier protein 5 (ADP/ATP translocase 5).
 GN TLCE OR TLCS OR RP739.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria.";
 RL Nature 396:133-140(1998).
 RN [2]
 RP SEQUENCE OF 325-500 FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=97419517; PubMed=9274032;
 RA Andersson J.O., Andersson S.G.E.,
 RT "Genomic rearrangements during evolution of the obligate
 RT intracellular parasite Rickettsia prowazekii as inferred from an
 RT analysis of 52015 bp nucleotide sequence.";
 RL Microbiology 143:2783-2795(1997).
 CC -I- FUNCTION: PROVIDES THE RICKETTSIAL CELL WITH HOST ATP IN
 CC EXCHANGE FOR RICKETTSIAL ADP. THIS IS AN OBLIGATE EXCHANGE SYSTEM.
 CC THIS ENERGY ACQUIRING ACTIVITY IS AN IMPORTANT COMPONENT OF
 CC RICKETTSIAL PARASITISM (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: BELONGS TO THE ADP/ATP TRANSLOCASE TLC FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; AJ235273; CAA15167.1; -;
 CC DR EMBL; Y11778; CAZ72457.1; -;
 CC DR InterPro; IPR004667; ADP_ATP_car.
 CC DR Pfam; PF03219; TLC; 1.
 CC DR TIGRFAMs; TIGR00769; AAA; 1.
 CC KW Transmembrane; Transport; ATP-binding; Multigene family;
 CC Complete proteome.
 CC FT TRANSMEM 26 46 POTENTIAL.
 CC FT TRANSMEM 52 82 POTENTIAL.
 CC FT TRANSMEM 94 114 POTENTIAL.
 CC FT TRANSMEM 149 169 POTENTIAL.
 CC FT TRANSMEM 184 204 POTENTIAL.
 CC FT TRANSMEM 224 244 POTENTIAL.
 CC FT TRANSMEM 287 307 POTENTIAL.
 CC FT TRANSMEM 328 348 POTENTIAL.
 CC FT TRANSMEM 357 377 POTENTIAL.
 CC FT TRANSMEM 381 401 POTENTIAL.
 CC FT TRANSMEM 469 489 POTENTIAL.
 CC SQ SEQUENCE 500 AA; 57073 MW; FE3DB48D08CF5F72 CRC64;

Query Match 63.2%; Score 43; DB 1; Length 500;
 Best Local Similarity 63.6%; Pred.No. 1.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAMQAMRKV 11
 DB 482 CFWAYAVRKI 492

RESULT 5

TRFL_MOUSE
 ID TRFL_MOUSE STANDARD; PRT; 707 AA.
 AC P08071; P70690; Q61799; Q9222P;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=87280033; PubMed=3611056;
 RA Pentecost B.T.; Teng C.T.;
 RT "Lactotransferrin is the major estrogen inducible protein of mouse
 uterine secretions."
 RL J. Biol. Chem. 262:10134-10139(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Morishita K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Straubeberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-14 FROM N.A.
 RX MEDLINE=92042099; PubMed=1939212;
 RA Liu Y.; Teng C.T.;
 RT "Characterization of estrogen-responsive mouse lactoferrin promoter."
 RL J. Biol. Chem. 266:21880-21895(1991).

CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -!- SUBUNIT: MONOMER.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 CC
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 CC
 CC EMBL; J03298; AAA40525.1; -
 CC EMBL; D88510; BAA13633.1; -
 CC EMBL; BC006904; AAH06904.1; -
 CC EMBL; M74778; AAA39427.1; -
 CC PIR; A28438; A28438.
 CC HSP; P02788; 1CE6.
 CC MGD; MGI:96837; Ltf.
 CC InterPro; IPR001156; Transferrin.
 CC Pfam; PF00405; transferrin; 2.
 CC PRINTS; PR00422; TRANSFERRIN.
 CC SMART; SM00094; TR_FER; 2.
 CC PROSITE; PS00205; TRANSFERRIN_1; 1.
 CC PROSITE; PS00206; TRANSFERRIN_2; 2.
 CC PROSITE; PS00207; TRANSFERRIN_3; 2.
 KW Transferrin; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.

FT SIGNAL 1 19
 FT CHAIN 20 707
 FT REPEAT 20 357
 FT REPEAT 358 707
 FT REPEAT 358 707
 FT DISULFID 27 63
 FT DISULFID 37 54
 FT DISULFID 133 216
 FT DISULFID 175 191
 FT DISULFID 188 199
 FT DISULFID 249 263
 FT DISULFID 366 398
 FT DISULFID 376 389
 FT DISULFID 423 702
 FT DISULFID 443 665
 FT DISULFID 475 550
 FT DISULFID 499 693
 FT DISULFID 509 523
 FT DISULFID 520 533
 FT DISULFID 591 605
 FT DISULFID 643 648
 FT METAL 78 78
 FT METAL 110 110
 FT METAL 210 210
 FT METAL 271 271
 FT METAL 413 413
 FT METAL 451 451
 FT METAL 544 544
 FT METAL 613 613
 FT BINDING 139 139
 FT BINDING 481 481
 FT CARBOHYD 118 118
 FT CARBOHYD 494 494
 FT CONFLICT 1 2
 FT CONFLICT 25 25
 FT CONFLICT 82 82
 FT CONFLICT 359 359
 FT CONFLICT 382 382
 FT CONFLICT 449 449
 FT CONFLICT 629 629
 SQ SEQUENCE 707 AA; 77865 MW; F26AE0340AC19A8 CRC64;
 Query Match 61.8%; Score 42; DB 1; Length 707;
 Best Local Similarity 63.6%; Pred. No. 3.1;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAMQAMRKV 11
 DB 37 CLRQWENRKV 47

RESULT 6

BUB2 YEAST
 ID BUB2 YEAST STANDARD; PRT; 306 AA.
 AC P2648;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).
 GN BUB2 OR YMR055C OR YMR796.08C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=91330299; PubMed=1651171;
 RA Hoyt M.A.; Totis L.; Roberts B.T.;
 RT "S. cerevisiae genes required for cell cycle arrest in response to
 loss of microtubule function."
 RL Cell 66:507-517(1991).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=9288C / AB972;
RA Devlin K., Churcher C.M., Barrall B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=21385309; PubMed=11493673;
RA Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Fesquet D.,
RA Johnston L.H.;
RT "the Bub2-dependent mitotic pathway in yeast acts every cell cycle and
RT regulates cytokinesis.";
RL J. Cell Sci. 114:2345-2354 (2001).
CC -1- FUNCTION: Part of a checkpoint which monitors spindle integrity
CC and prevents premature exit from mitosis. This cell-cycle arrest
CC depends upon inhibition of the G-protein Tem1 by the BFA1/BUB2
CC complex.
CC -1- SUBUNIT: Interacts with BFA1.
CC -1- SUBCELLULAR LOCATION: Spindle poles.
CC -1- SIMILARITY: TO S.POMBE CDC16.
CC -----
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CC -----
CC EMBL; M64706; AAA16885.1; -;
CC EMBL; Z49703; CAA89765.1; -;
CC PIR; A39654; A39654.
CC SGD; S0004659; BUB2.
CC InterPro; IPR000195; RabGAP_TBC.
CC Pfam; PF00566; TBC; 1.
CC SMART; SM00164; TBC; 1.
CC Cell cycle; Mitosis.
CC SEQUENCE 306 AA; 35027 MW; A1DDBPB548E81EA3 CRC64;

Query Match 58.8%; Score 40; DB 1; Length 306;
Best Local Similarity 60.0%; Pred. No. 3.1;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQAMRK 10
DB 108 CFAWQTOQR 117

RESULT 7
ID PHYC SORBI STANDARD; PRT; 1135 AA.
AC P93528;
DT 16-OCT-2001 (Rel. 40, Created)
DT 18-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome C.
DE PHYC.
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97198556; PubMed=9046599;
RA Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
RA Morgan P.W., Muller J.E.;
RT "The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
RT phytochrome B.";
RL Plant Physiol. 113:611-619 (1997).
CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT. THE PR FORM THAT ABSORBS
CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS

CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, THE
CC PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS THE
CC EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY
CC SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- PFM: CONTAINS ONE COVALENTLY LINKED TETRAPEPTIDE CHROMOPHORE.
CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC -----
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CC -----
CC EMBL; U56731; AAB41399.1; -;
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR003018; GAF.
CC InterPro; IPR004359; HIS_KIN_sig.
CC InterPro; IPR003661; His_KIN.
CC InterPro; IPR001610; PAC.
CC InterPro; IPR000014; PAS domain.
CC InterPro; IPR001294; Phytochrome.
CC Pfam; PF00360; Phytochrome; 1.
CC Pfam; PF00512; signal; 1.
CC Pfam; PF00989; PAS; 2.
CC Pfam; PF01590; GAF; 1.
CC Pfam; PF02518; HATPase_c; 1.
CC PRINTS; PR01033; PHYTOCHROME.
CC SMART; SM00065; GAF; 1.
CC SMART; SM00387; HATPase_c; 1.
CC SMART; SM00388; HSKA; 1.
CC SMART; SM00086; PAC; 1.
CC SMART; SM00091; PAS; 2.
CC TIGRfam; TIGR00229; sensory_box; 2.
CC PROSITE; PS0109; HIS_KIN; 1.
CC PROSITE; PS0112; PAS; 2.
CC PROSITE; PS00245; PHYTOCHROME_1; FALSE_NEG.
CC PROSITE; PS0046; PHYTOCHROME_2; 1.
CC Repeat; Multigene family.
CC Repeat; Multigene family.
CC FT DOMAIN 618 688 PAS 1.
CC FT DOMAIN 748 822 PAS 2.
CC FT DOMAIN 902 1122 HISTIDINE KINASE.
CC FT BINDING 321 321 CHROMOPHORE (BY SIMILARITY).
CC SEQUENCE 1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;

Query Match 57.4%; Score 39; DB 1; Length 1135;
Best Local Similarity 45.5%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFAWQAMRKV 11
DB 775 CLEWNAKMKI 785

RESULT 8
ID IL2A BOVIN STANDARD; PRT; 275 AA.
AC P12342;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
DE subunit) (P55) (TAC antigen) (CD25).
GN IL2RA.

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8212503; PubMed=2835311;
RA Weinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
RA Reeves R., Magnuson J.A.;
RT "Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
RL Immunology 63:603-610(1986).
RN [2]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=96115968; PubMed=8563178;
RA Yoo J., de Leon F.A., Stone R.T., Beattie C.W.;
RT "Cloning and chromosomal assignment of the bovine interleukin-2
receptor alpha (IL-2R alpha) gene.";
RL Mamm. Genome 6:751-753(1995).
CC -!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
WITH A GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
CC
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CC
CC EMBL; M20818; AA51414.1; -;
CC EMBL; U24226; AAC48487.1; -;
CC PIR; S07442; S07442.
CC HSSP; P01589; IILM.
CC InterPro: IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00084; sushi; 2.
CC SMART; SM00032; CCP; 2.
CC Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
FT SIGNAL 1 21
FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 262 POTENTIAL.
FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 223 278 SUSHI 1.
FT DOMAIN 122 185 SUSHI 2.
FT DISULFID 24 64 BY SIMILARITY.
FT DISULFID 751 77 BY SIMILARITY.
FT DISULFID 123 168 BY SIMILARITY.
FT DISULFID 152 184 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 275 AA; 31238 MW; 4901BBF9A4862390 CRC64;
Query Match 54.4%; Score 37; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 CFAWORAMRKVR 12
Db 261 CLTWQRWKVKR 272
RESULT 9
IL2A_SHEEP STANDARD; PRT; 275 AA.
ID IL2A_SHEEP
AC P28698;
DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
subunit) (P55) (TAC antigen) (CD25).
GN IL2RA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92241602; PubMed=1572550;
RA Bu'doso R., Sargan D.R., Williamson M.L., McConnell I.;
RT "Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa
protein, CD25.";
RL Gene 113:283-284(1992).
CC -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
WITH A GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; Z11560; CAA77652.1; -;
CC EMBL; X60149; CAA42723.1; -;
CC EMBL; A19167; CAA01447.1; -;
CC PIR; S18910; S18910.
CC PIR; S18899; S18899.
CC PIR; JC1113; JC1113.
CC HSSP; P01589; IILM.
CC InterPro: IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00084; sushi; 2.
CC SMART; SM00032; CCP; 2.
CC Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
FT SIGNAL 1 21
FT CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 262 POTENTIAL.
FT DOMAIN 263 275 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 223 278 SUSHI 1.
FT DOMAIN 122 185 SUSHI 2.
FT DISULFID 24 64 BY SIMILARITY.
FT DISULFID 751 77 BY SIMILARITY.
FT DISULFID 123 168 BY SIMILARITY.
FT DISULFID 152 184 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 166 166 S -> T (IN REF. 2).
SQ SEQUENCE 275 AA; 30904 MW; 1101A2DESACS088 CRC64;
Query Match 54.4%; Score 37; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 CFAWORAMRKVR 12
Db 261 CLTWQRWKVKR 272

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RESULT 10
ID UL24_HSVSA STANDARD; PRT; 303 AA.
AC Q01005;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Gene 20 protein.
GN 20.
OS Herpesvirus saimiri (strain 11).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
CX NCBI_TaxID=10383;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333688; PubMed=1321287;
RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
RA Honess R.W.;
RT "Primary structure of the herpesvirus saimiri genome.";
RL J. Virol. 66:5047-5058(1992).
CC -/- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL24,
CC - EHV-1 37, EBV BXRFL, HCMV UL76, ILTV ORF3, AND VZV 35.
CC
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CC
CC EMBL; X64346; CAA45644.1; -
CC
CC PIR; B36808; WZBEM6.
CC InterPro: IPR002580; Herpes UL24.
CC Pfam: PF01646; Herpes UL24; 1.
CC SEQUENCE 303 AA; 34942 MW; DF6D59F7A1C93A0B CRC64;
CC
CC Query Match 54.4%; Score 37; DB 1; Length 303;
CC Best Local Similarity 50.0%; Pred. No. 11;
CC Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
CC
CC QY 1 CFANQRAMRKVR 12
CC ||| ||| ||| |||
CC Db 174 CFLWSRADVEIR 185
CC
CC RESULT 11
ID WD66_PHYPO STANDARD; PRT; 601 AA.
AC P90587;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 66 kDa stress protein (p66).
OS Physarum polycephalum (Slime mold).
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
OC Physarum.
CX NCBI_TaxID=5791;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98351989; PubMed=9685722;
RA Matsumoto S., Ogawa M., Kasakura T., Shimada Y., Mitsui M., Maruya M.,
RA Isobata M., Yahara I., Murakami-Murofushi K.;
RT "A novel 66-kDa stress protein, p66, associated with the process of
RT cyst formation of Physarum polycephalum is a Physarum homologue of a
RT yeast actin-interacting protein, Aip1.";
RL J. Biochem. 124:326-331(1998).
CC -/- FUNCTION: ASSOCIATED WITH THE PROCESS OF CYST FORMATION.
CC -/- SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS).
CC -/- SIMILARITY: BELONGS TO THE AIP1 FAMILY OF WD-REPEAT PROTEINS.
CC

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CC
CC EMBL; U86011; AAC26321.1; -
CC InterPro: IPR001880; WD40.
CC Pfam: PF00400; WD40; 10.
CC SMART; PRO0320; GPROTEINBRPT.
CC PRINTS; SM00320; WD40; 10.
CC PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
CC PROSITE; PS50082; WD_REPEATS_2; 6.
CC PROSITE; PS50294; WD_REPEATS_REGION; 1.
CC Repeat; WD repeat.
KW REPEAT 56 95 WD 1.
FT REPEAT 100 143 WD 2.
FT REPEAT 145 184 WD 3.
FT REPEAT 187 226 WD 4.
FT REPEAT 233 272 WD 5.
FT REPEAT 318 357 WD 6.
FT REPEAT 435 478 WD 7.
FT REPEAT 483 522 WD 8.
FT REPEAT 526 565 WD 9.
FT REPEAT 569 600 WD 10.
SQ SEQUENCE 601 AA; 64321 MW; P691217D838F747A CRC64;
CC
CC Query Match 54.4%; Score 37; DB 1; Length 601;
CC Best Local Similarity 45.5%; Pred. No. 23;
CC Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 2 FAWQRAMRKVR 12
CC ||| ||| ||| |||
CC Db 510 FVWDKASRKIK 520
CC
CC RESULT 12
ID PHYC_ORYSA STANDARD; PRT; 1137 AA.
AC Q9ZWI9; P93429;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytochrome C.
GN PHYC.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
CX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Tahir M., Kanegae H., Takano M.;
RT "Phytochrome C (PHYC) gene in rice: isolation and characterization of
RT a complete coding sequence.";
RL (in) Plant Gene Register PGR98-210.
RN [2]
RP SEQUENCE OF 275-378 FROM N.A.
RX MEDLINE=97019052; PubMed=8865668;
RA Mathews S., Sharrock R.A.;
RT "The phytochrome gene family in grasses (Poaceae): a phylogeny and
RT evidence that grasses have a subset of the loci found in dicot
RT angiosperms.";
RL Mol. Biol. Evol. 13:1141-1150(1996).
CC -/- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE

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CC RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
 CC GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
 CC BIPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
 CC PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS
 CC THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPEPTIDE CHROMOPHORE.
 CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
 CC
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 CC
 CC EMBL; AB018442; BAA74448.1; -
 CC EMBL; U61207; ABA41996.1; -
 CC InterPro; IPR003594; ATPbind_ATPase.
 CC InterPro; IPR003018; GAR.
 CC InterPro; IPR004359; HIS_KIN_sig.
 CC InterPro; IPR003661; His_kinA.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS domain.
 CC InterPro; IPR001294; Phytochrome.
 CC Pfam; PF00360; phytochrome; 1.
 CC Pfam; PF00512; signal; 1.
 CC Pfam; PF00989; PAS; 2.
 CC Pfam; PF01590; GAR; 1.
 CC Pfam; PF02518; HATPase_c; 1.
 CC PRINTS; PR01033; PHYTOCHROME.
 CC SMART; SM00065; GAR; 1.
 CC SMART; SM00387; HATPase_c; 1.
 CC SMART; SM00388; HSKA; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 2.
 CC TIGRFAMs; TIGR00229; sensory_box; 2.
 CC PROSITE; PS50109; HIS_KIN; 1.
 CC PROSITE; PS50112; PAS_2.
 CC PROSITE; PS00245; PHYTOCHROME_1; 1.
 CC PROSITE; PS50046; PHYTOCHROME_2; 1.
 CC Repeat; Multigene family.
 CC Domain; 620 690 PAS 1.
 CC Domain; 750 824 PAS 2.
 CC Domain; 904 1124 HISTIDINE KINASE.
 CC BINDING 322 322 CHROMOPHORE (BY SIMILARITY).
 CC CONFLICT 279 279 F -> S (IN REF. 2).
 CC CONFLICT 292 292 C -> S (IN REF. 2).
 CC SEQUENCE 1137 AA; 125982 MW; F2A520181CFE7B32 CRC64;
 CC
 CC Query Match 54.4%; Score 37; DB 1; Length 1137;
 CC Best Local Similarity 45.5%; Pred. No. 44;
 CC Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 1 CFAWRAMRKV 11
 CC DB 777 CLENNEMQKI 787
 CC
 CC RESULT 13
 CC ATX1_ARATH STANDARD; PRT; 1179 AA.
 CC AC Q9LTO2;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Potential cation-transporting ATPase (EC 3.6.3.-).
 CC GN A15G23630 OR MQM1.11.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eursids II; Brassicales; Brassicaceae; Arabidopsi.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=sv. Columbia;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty pl and TAC
 RL clones.";
 RL DNA Res. 7:31-63(2000).
 CC -1- FUNCTION: INVOLVED IN TRANSPORT OF CATIONS (POTENTIAL).
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (E1-E2 ATPASES). SUBFAMILY V.
 CC
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 CC
 CC EMBL; AB025633; BAA97238.1; -
 CC InterPro; IPR001757; ATPase_E1-E2.
 CC InterPro; IPR001454; H1gnase/hydrlase.
 CC Pfam; PF00122; E1-E2_ATPase; 1.
 CC Pfam; PF00702; Hydrolase_1.
 CC PRINTS; PR00119; CAIATPASE.
 CC PROSITE; PS00154; ATPASE_E1_E2; 1.
 CC Hydrolase; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
 CC Magnesium.
 CC Domain; 1 20 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 21 42 POTENTIAL.
 CC Domain; 43 50 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 51 71 POTENTIAL.
 CC Domain; 72 192 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 193 215 POTENTIAL.
 CC Domain; 216 218 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 219 238 POTENTIAL.
 CC Domain; 239 402 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 403 422 POTENTIAL.
 CC Domain; 423 435 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 436 453 POTENTIAL.
 CC Domain; 454 947 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 948 967 POTENTIAL.
 CC Domain; 968 979 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 980 997 POTENTIAL.
 CC Domain; 998 1013 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 1014 1034 POTENTIAL.
 CC Domain; 1035 1059 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 1060 1079 POTENTIAL.
 CC Domain; 1080 1092 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 1093 1110 POTENTIAL.
 CC Domain; 1111 1128 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 1129 1148 POTENTIAL.
 CC Domain; 1149 1179 POTENTIAL.
 CC TRANSMEM 1175 1178 CYTOPLASMIC (POTENTIAL).
 CC Domain; 812 812 POLY-LYS.
 CC TRANSMEM 816 816 PHOSPHORYLATION (BY SIMILARITY).
 CC METAL 812 812 MAGNESIUM (BY SIMILARITY).
 CC METAL 816 816 MAGNESIUM (BY SIMILARITY).
 CC SEQUENCE 1179 AA; 131115 MW; 4A3E82D222A4D78 CRC64;
 CC
 CC Query Match 54.4%; Score 37; DB 1; Length 1179;
 CC Best Local Similarity 44.4%; Pred. No. 45;
 CC Matches 4; Conservative 1; Indels 0; Gaps 0;

QY 1 CRAWFORD 9
DB 1144 CYSWERLER 1152

RESULT 14
ID ABRH HUMAN STANDARD, PRT; 2273 AA.
AC P78363. 060438; 060915; 015112;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Retinal-specific ATP-binding cassette transporter (RIM ABC
DE transporter) (RIM protein) (RMP) (Stargardt disease protein).
GN ABCA4 OR ABCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A., VARIANTS STGD, AND VARIANTS HIS-846 AND GLN-943.
RP MEDLINE=97207541; PubMed=9054934;
RA Allikmets R., Singh N., Sun H., Shroyer N.F., Hutchinson A.,
RA Chidambaram A., Gerard B., Baird L., Stauffer D., Peiffer A.,
RA Ratnaker A., Smallwood P.M., Li Y., Anderson K.L., Lewis R.A.,
RA Nathans J., Leppert M., Dean M., Lupski J.R.;
RT "A photoreceptor cell-specific ATP-binding transporter gene (ABCR) is
RT mutated in recessive Stargardt macular dystrophy.";
RL Nat. Genet. 15:236-246 (1997).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=97345663; PubMed=9202155;
RA Azarian S.M., Travis G.H.;
RT "The photoreceptor rim protein is an ABC transporter encoded by the
RT gene for recessive Stargardt's disease (ABCR).";
RL FEBS Lett. 409:247-252 (1997).
RN [3]
RN SEQUENCE FROM N.A., AND VARIANTS STGD TRP-18 AND CYS-212.
RP MEDLINE=98163759; PubMed=9503029;
RA Gerber S., Rozet J.-M., van de Pol T.J.R., Hoyng C.B., Munnich A.,
RA Blankenagel A., Kaplan J., Cremers F.P.M.;
RT "Complete exon-intron structure of the retina-specific ATP binding
RT transporter gene (ABCR) allows the identification of novel mutations
RT underlying Stargardt disease.";
RL Genomics 48:139-142 (1998).
RN [4]
RN SEQUENCE FROM N.A., AND VARIANTS STGD.
RP MEDLINE=98141123; PubMed=9490294;
RA Nasonkin I., Illing M., Koehler M.R., Schmid M., Molday R.S.,
RA Weber B.H.F.;
RT "Mapping of the rod photoreceptor ABC transporter (ABCR) to 1p21-p22.1
RT and identification of novel mutations in Stargardt's disease.";
RL Hum. Genet. 102:21-26 (1998).
RN [5]
RN CHARACTERIZATION.
RP MEDLINE=99175213; PubMed=10075733;
RA Sun H., Molday R.S., Nathans J.;
RT "Retinal stimulates ATP hydrolysis by purified and reconstituted ABCR,
RT the photoreceptor-specific ATP-binding cassette transporter
RT responsible for Stargardt disease.";
RL J. Biol. Chem. 274:8269-8281 (1999).
RN [6]
RN DISEASE.
RP MEDLINE=98133912; PubMed=9466990;
RA Cremers F.P.M., van de Pol D.J.R., van Driel M.A., den Hollander A.I.,
RA van Haren F.J.J., Koenen N.V.A.M., Tijmes N., Bergen A.A.B.,
RA Rohrschneider K., Blankenagel A., Pinkers A.J.L.G., Deutman A.F.,
RA Hoyng C.B.;
RT "Autosomal recessive retinitis pigmentosa and cone-rod dystrophy
RT caused by splice site mutations in the Stargardt's disease gene
RT ABCR.";
RL Hum. Mol. Genet. 7:355-362 (1998).
RN [7]

RP VARIANTS ARMD2, AND VARIANTS.
RX MEDLINE=9742530; PubMed=9295268;
RA Allikmets R., Shroyer N.F., Singh N., Seddon J.M., Lewis R.A.,
RA Bernstein P.S., Peiffer A., Zabriskie N.A., Li Y., Hutchinson A.,
RA Dean M., Lupski J.R., Leppert M.;
RT "Mutation of the Stargardt disease gene (ABCR) in age-related macular
RT degeneration.";
RL Science 277:1805-1807 (1997).
RN [8]
RN VARIANTS STGD W-18; C-212; H-636; M-1019; V-1038; C-1108; W-1640;
RP S-1977 AND H-2107, AND VARIANTS FFM P-11; P-341; V-1038; E-1091;
RP C-1508; F-1970 AND R-1971.
RX MEDLINE=98454319; PubMed=9781034;
RA Rozet J.-M., Gerber S., Souied E., Perrault I., Chatelin S., Ghazi I.,
RA Lewski C., Dufier J.-L., Munnich A., Kaplan J.;
RT "Spectrum of ABCR gene mutations in autosomal recessive macular
RT dystrophies.";
RL Eur. J. Hum. Genet. 6:291-295 (1998).
RN [9]
RN VARIANTS STGD.
RP MEDLINE=99138655; PubMed=9973280;
RA Lewis R.A., Shroyer N.F., Singh N., Allikmets R., Hutchinson A.,
RA Li Y., Lupski J.R., Leppert M., Dean M.;
RT "Genotype/phenotype analysis of a photoreceptor-specific ATP-binding
RT cassette transporter gene, ABCR, in Stargardt disease.";
RL Am. J. Hum. Genet. 64:422-434 (1999).
RN [10]
RN VARIANTS STGD, AND VARIANTS.
RX MEDLINE=99192348; PubMed=10090887;
RA Maugeri A., van Driel M.A., van de Pol D.J.R., Klevering B.J.,
RA van Haren F.J.J., Tijmes N., Bergen A.A.B., Rohrschneider K.,
RA Blankenagel A., Pinkers A.J.L.G., Dahl N., Brunner H.G.,
RA Deutman A.F., Hoyng C.B., Cremers F.P.M.;
RT "The 2588G->C mutation in the ABCR gene is a mild frequent founder
RT mutation in the western European population and allows the
RT classification of ABCR mutations in patients with Stargardt disease.";
RL Am. J. Hum. Genet. 64:1024-1035 (1999).
RN [11]
RN VARIANTS STGD TYR-54, AND VARIANT ALA-863.
RX MEDLINE=20077755; PubMed=10612508;
RA Zhang K., Garibaldi D.C., Khazava M., Albini T., Chiang M.F.,
RA Kerrigan M., Sunness J.S., Han M., Allikmets R.;
RT "A novel mutation in the ABCR gene in four patients with autosomal
RT recessive Stargardt disease.";
RL Am. J. Ophthalmol. 128:720-724 (1999).
RN [12]
RN VARIANTS STGD V-60; R-206; N-300; P-541; A-849; P-974; V-1038; C-1108;
RP L-1408; R-1488; D-1652; P-1729; E-1961; W-2038; W-2077; H-2107; R-2128
RP AND Y-2150.
RX MEDLINE=99221420; PubMed=10206579;
RA Fiehan G.A., Stone E.M., Grover S., Derlacki D.J., Haines H.L.,
RA Hockey R.R.;
RT "Variation of clinical expression in patients with Stargardt dystrophy
RT and sequence variations in the ABCR gene.";
RL Arch. Ophthalmol. 117:504-510 (1999).
RN [13]
RN VARIANTS GLU-1961 AND ASN-2177.
RX MEDLINE=20349288; PubMed=10830298;
RA Allikmets R., Tamur J., Hutchinson A., Lewis R.A., Shroyer N.F.,
RA Datskikhvili K., Lupski J.R., Steiner K., Pauleikhoff D., Holz F.G.,
RA Weber B.H.F., Dean M., Atkinson A., Gail M.H., Bernstein P.S.,
RA Singh N., Peiffer A., Zabriskie N.A., Leppert M., Seddon J.M.,
RA Zhang K., Sunness J.S., Udar N.S., Velchits S., Silva-Garcia R.,
RA Small K.W., Simonelli F., Testa F., D'Urso M., Brancato R.,
RA Rinaldi E., Ingavst J.J.M., ten Brink J.B., de Jong P.T.V.M.,
RA Kaplan J., Assink J.J.M., van Driel M.A., Hoyng C.B., Cremers F.P.M.,
RA Bergen A.A.B., Maugeri A., van Haren F.J.J., Deutman A.F.,
RA Paloma E., Chot R., Balcells S., Gonzalez-Duarte R., Kermani S.,
RA Stanga P., Bhatnagar S.S., Bird A.C.;
RT "Further evidence for an association of ABCR alleles with age-related
RT macular degeneration.";
RL Am. J. Hum. Genet. 67:487-491 (2000).
RN [14]

RP VARIANTS STGD E-60; T-60; E-65; L-68; R-72; C-212; S-230; S-247;
 RP V-328; K-471; P-541; Q-572; R-607; K-635; C-653; Y-764; R-765; A-901;
 RP I-959; K-1036; V-1038; P-1063; D-1087; C-1108; L-1380; K-1399;
 RP P-1430; V-1440; L-1486; Y-1488; M-1537; P-1689; L-1705;
 RP T-1733; R-1748; P-1763; K-1885; H-1898; B-1961; R-1975; S-1977; G-2077
 RP W-2077 AND V-2241. AND VARIANTS Q-152; H-212; R-423; I-552; R-914;
 RP Q-943; T-1562; I-1868; M-1921; L-1948; F-1970; A-2059; N-2177 AND
 RP V-2216.
 RX MEDLINE=20442027; PubMed=10958763;
 RA Rivera A., White K., Stoehr H., Steiner K., Hemmrich N., Grimm T.,
 RA Jurkies B., Lorenz B., Scholl H.P.N., Apfelstedt-Sylla E.,
 RA Weber B.H.F.;
 RT "A comprehensive survey of sequence variation in the ABCA4 (ABCR) gene
 RT in Stargardt disease and age-related macular degeneration.";
 RL Am. J. Hum. Genet. 67:800-813(2000).
 RN [15]
 RP VARIANTS CORD3 GLN-65; CYS-212; PRO-541; ALA-863; GLY-863 DEL;
 RP VAL-1038; LYS-1122; TYR-1490 AND ASP-1598.
 RX MEDLINE=20442040; PubMed=10958761;
 RA Maugeri A., Klavering B.J., Rohrschneider K., Blankensgel A.,
 RA Brunner H.G., Deutman A.F., Hoyng C.B., Cremers F.P.M.;
 RT "Mutations in the ABCA4 (ABCR) gene are the major cause of autosomal
 RT recessive cone-rod dystrophy.";
 RL Am. J. Hum. Genet. 67:960-966(2000).
 RN [16]
 RP VARIANTS STGD ASP-340; GLN-572; ALA-863; SER-965; VAL-1038; ALA-1780
 RP AND HIS-1898, AND VARIANT GLN-943.
 RX MEDLINE=20208356; PubMed=10746567;
 RA Shroyer N.F., Lewis R.A., Lupski J.R.;
 RT "Complex inheritance of ABCR mutations in Stargardt disease: linkage
 RT disequilibrium, complex alleles, and pseudodominance";
 RL Hum. Genet. 106:244-248(2000).
 RN [17]
 RP VARIANTS STGD.
 RX MEDLINE=20095082; PubMed=10634594;
 RA Papaioannou M., Osaka L., Bessant D., Lois N., Bird A.C., Payne A.,
 RA Bhattacharya S.S.;
 RT "An analysis of ABCR mutations in British patients with recessive
 RT retinal dystrophies";
 RL Invest. Ophthalmol. Vis. Sci. 41:16-19(2000).
 RN [18]
 RP VARIANTS STGD C-212; D-767; I-897; V-1038; K-1087; K-1399; Q-1640 AND
 RP E-1961, AND VARIANT HIS-212.
 RX MEDLINE=20174852; PubMed=10711710;
 RA Simonelli F., Testa F., de Creschio G., Rinaldi E., Hutchinson A.,
 RA Atkinson A., Dean M., D'Urso M., Allikmets R.;
 RT "New ABCR mutations and clinical phenotype in Italian patients with
 RT Stargardt disease";
 RL Invest. Ophthalmol. Vis. Sci. 41:892-897(2000).
 RN [19]
 RP CHARACTERIZATION OF VARIANTS, AND MUTAGENESIS OF GLY-966; LYS-969;
 RP GLY-1975 AND LYS-1978.
 RX MEDLINE=20472331; PubMed=11017087;
 RA Sun H., Smallwood F.W., Nathans J.;
 RT "Biochemical defects in ABCR protein variants associated with human
 RT retinopathies";
 RL Nat. Genet. 26:242-246(2000).
 RN [20]
 RP VARIANT STGD ASN-972, AND VARIANTS GLN-943; ILE-1868 AND LEU-1948.
 RX MEDLINE=21478761; PubMed=11594933;
 RA Eksandh L., Ekstrom U., Abrahamson M., Bauer B., Andreasson S.;

Query Match 54.4%; Score 37; DB 1; Length 2273;
 Best Local Similarity 75.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CFAWQAM 8
 Db 779 CFAWQDM 786

RESULT 15
 DYHB_CHLRE

ID DYHB_CHLRE STANDARD; PRT; 4568 AA.
 AC Q39565;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DB Dynein beta chain, flagellar outer arm.
 OS ODA4 OR ODA-4 OR SUP1.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadales; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=21gr;
 RX MEDLINE=94274778; PubMed=8006077;
 RA Mitchell D.R., Brown K.S.;
 RT "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
 RT chain genes.";
 RL J. Cell Sci. 107:635-644(1994).
 CC -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
 CC FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
 CC DYNEIN HAS ATPASE ACTIVITY.
 CC -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
 CC GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
 CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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 CC -----
 DR EMBL; U02963; AAA19956.1; -
 DR InterPro; IPR004273; Dynein heavy.
 DR Pfam; PF03028; Dynein heavy; 1.
 KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
 KM Coiled coil.
 FT Coiled coil.. 277 293
 FT DOMAIN 1158 1175 COILED COIL (POTENTIAL).
 FT DOMAIN 1372 1400 COILED COIL (POTENTIAL).
 FT DOMAIN 1614 1650 COILED COIL (POTENTIAL).
 FT DOMAIN 1778 1825 COILED COIL (POTENTIAL).
 FT DOMAIN 2017 2045 MICROTUBULE-BINDING (POTENTIAL).
 FT DOMAIN 2831 2848 COILED COIL (POTENTIAL).
 FT DOMAIN 3106 3162 COILED COIL (POTENTIAL).
 FT DOMAIN 3648 3728 COILED COIL (POTENTIAL).
 FT NP_BIND 1919 1926 ATP (POTENTIAL).
 FT NP_BIND 2202 2209 ATP (POTENTIAL).
 FT NP_BIND 2530 2537 ATP (POTENTIAL).
 FT NP_BIND 2879 2886 ATP (POTENTIAL).
 SQ SEQUENCE 4568 AA; 519961 MW; 9A9A5393C7C36AE7 CRC64;

Query Match 54.4%; Score 37; DB 1; Length 4568;
 Best Local Similarity 41.7%; Pred. No. 1.8e+02;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CFAWQAMKVR 12
 Db 1852 CFQWQSLRYIQ 1863

Search completed: February 21, 2003, 07:51:42
 Job time : 6.2093 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
(without alignments)
114.078 Million cell updates/sec

Title: US-09-743-107b-95
Perfect score: 68
Sequence: 1 CFAWQRMKRV 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	76.5	711	4 Q8TCD2	Q8Tcd2 homo sapien
2	48	70.6	38	4 Q9UCY5	Q9ucy5 homo sapien
3	44	64.7	33	6 Q9TR80	Q9tr80 ovis aries
4	42	61.8	121	16 Q8U6K3	Q8u6k3 agrobacteri
5	40	58.8	114	11 Q83104	Q83104 rattus norv
6	40	58.8	234	11 Q83112	Q83112 rattus norv
7	39	57.4	511	16 Q8Z462	Q8z462 salmonella
8	39	57.4	1121	10 Q9SWS6	Q9sws6 lycopersico
9	38	55.9	134	2 Q87054	Q87054 vibrio chol
10	38	55.9	289	10 Q9C6N2	Q9c6n2 arabidopsis
11	38	55.9	329	16 Q98GW4	Q98gw4 rhizobium l
12	38	55.9	561	16 Q9KXK6	Q9kxk6 vibrio chol
13	38	55.9	759	4 Q9BVH6	Q9bvh6 homo sapien
14	38	55.9	1265	4 Q9P2G7	Q9p2g7 homo sapien
15	38	55.9	1417	4 Q9NYF4	Q9nyf4 homo sapien
16	38	55.9	1581	4 Q9BW93	Q9bw93 homo sapien

17	38	55.9	1787	4 Q9UPS0	Q9ups0 homo sapien
18	37	54.4	161	16 Q8U6L8	Q8u6l8 agrobacteri
19	37	54.4	202	16 Q83603	Q83603 treponema p
20	37	54.4	205	16 Q986A0	Q986a0 rhizobium l
21	37	54.4	206	16 Q8UHC2	Q8uhc2 agrobacteri
22	37	54.4	206	16 Q92RH8	Q92rh8 rhizobium m
23	37	54.4	208	16 Q8YFK3	Q8yfk3 brucella me
24	37	54.4	233	2 Q9AJ90	Q9aj90 actinobacil
25	37	54.4	292	2 Q9JRR3	Q9jrr3 actinobacil
26	37	54.4	292	2 Q9AQB8	Q9aqb8 actinobacil
27	37	54.4	294	2 Q6G251	Q6g251 actinobacil
28	37	54.4	303	12 Q40640	Q40640 saimirine
29	37	54.4	303	12 Q92585	Q92585 saimirine
30	37	54.4	337	16 Q8UJL5	Q8ujl5 agrobacteri
31	37	54.4	408	17 Q8ZVY6	Q8zvy6 pyrobaculum
32	37	54.4	484	13 Q9DGD7	Q9dgd7 oryzias lat
33	37	54.4	494	16 Q9HY41	Q9hy41 pseudomonas
34	37	54.4	499	16 Q92GI5	Q92gi5 rickettsia
35	37	54.4	502	10 Q65237	Q65237 arabidopsis
36	37	54.4	584	17 Q9HPA3	Q9hpa3 halobacteri
37	37	54.4	676	5 Q9N4T5	Q9n4t5 caenorhabdi
38	37	54.4	676	10 Q9FG26	Q9fg26 arabidopsis
39	37	54.4	737	5 Q95QJ8	Q95qj8 caenorhabdi
40	37	54.4	830	10 Q945T7	Q945t7 hordeum vul
41	37	54.4	1137	10 Q9M7A9	Q9m7a9 oryza sativ
42	37	54.4	1139	10 Q8VWNL	Q8vwnl triticum ae
43	37	54.4	1836	16 Q9PEL7	Q9pel7 xyella fas
44	37	54.4	2310	11 Q35600	Q35600 mus musculu
45	37	54.4	2858	5 Q9GYP6	Q9gyp6 caenorhabdi

ALIGNMENTS

RESULT 1

Q8TCD2 ID Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022347; AAH22347.1; -
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 76.5%; Score 52; DB 4; Length 711;
Best Local Similarity 81.8%; Pred. NO. 0.49;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 11
DB 39 CFAWQRMKRV 49

RESULT 2

Q9UCY5 ID Q9UCY5 PRELIMINARY; PRT; 38 AA.
AC Q9UCY5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Lactoferrin homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RA	Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deachrage G., Gillet W., Grant C., Kutayvin T., Levy R., Li M.-J., McClelland E., Palmeri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
RA	"The genome of the natural genetic engineer Agrobacterium tumefaciens C58";
RT	Science 294:2317-2323(2001).
RL	ENBL; A5009409; AA45598.1; --
DR	Hypothetical protein; Complete proteome.
KW	SEQUENCE 121 AA; 14085 MW; EBAF41617A3CEA53 CRC64;
SQ	
QY	Query Match 61.8%; Score 42; Length 121;
DB	Best Local Similarity 63.8%; Pred. No. 4.8;
	Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps
	1 CFANQQRMRKV 11
	:
	14 CLAWQRRNRV 24
RESULT 5	
Q63104	PRELIMINARY; PRT; 114 AA.
ID	Q63104
AC	Q63104;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DD	01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Carcinoembryonic antigen (Fragment).
GN	CEA4
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
ON	NCBI_TaxID=10116;
RX	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-ED II; TISSUE=LIVER;
RX	MEDLINE=89214106; PubMed=2708349;
RA	Kodelja V., Lucas K., Barnett S., von Kleist S., Thompson J.A., Zimmermann W.A.;
RT	"Identification of a carcinoembryonic antigen gene family in the rat: Analysis of the N-terminal domains reveals immunoglobulin-like, hypervariable regions.";
RT	J. Biol. Chem. 264:6906-6912(1989).
DR	ENBL; W60026; AAA40911.1; --
DR	NON_TER 1
SQ	SEQUENCE 114 AA; 12832 MW; 3AE10869B9B061686 CRC64;
QY	Query Match 58.8%; Score 40; DB 11; Length 114;
DB	Best Local Similarity 60.0%; Pred. No. 10;
	Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps
	2 FANQQRMRKV 11
	:
	42 FAWYGRLEKI 51
RESULT 6	
Q63112	PRELIMINARY; PRT; 234 AA.
ID	Q63112
AC	Q63112;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DD	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Carcinoembryonic antigen-related protein (Fragment).
GN	CGM4.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
ON	NCBI_TaxID=10116;

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RN  SEQUENCE FROM N.A.
RC  STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RA  Rebeck S., Lucas K., Thompson J.A., Zimmermann W.A.;
RL  Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
RN  [2]
RN  SEQUENCE FROM N.A.
RC  STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RA  MEDLINE=90243655; PubMed=2335509;
RX  Rebeck S., Lucas K., Thompson J.A., Zimmermann W.;
RT  "cDNA and gene analyses imply a novel structure for a rat
RL  carcinoembryonic antigen-related protein.";
RJ  J. Biol. Chem. 265:7872-7879(1990).
DR  EMBL: M32475; AAA66038.1;
DR  InterPro; IPR003599;
DR  InterPro; IPR003599;
DR  Pfam; PF00047;
DR  SMART; SM00409;
FT  NON TER 1
SQ  SEQUENCE 234 AA; 26171 MW; 69B9C9BE0C773F2A CRC64;

Query Match 58.8%; Score 40; DB 11; Length 234;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FAWQRMKRV 11
DB 42 FAWYGLRGI 51

RESULT 7
ID Q82462 PRELIMINARY; PRT; 511 AA.
AC Q82462;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Hypothetical protein STY3070.
GN STY3070.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;

[1]
RN  SEQUENCE FROM N.A.
RC  STRAIN=CT18;
RX  MEDLINE=21534947; PubMed=11677608;
RA  Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA  Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA  Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA  Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA  Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA  Krogh A., Larsen T.S., Leather S., Moule S., O'Goara P., Parry C.,
RA  Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA  Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627276; CAD06049.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 511 AA; 58136 MW; E2DD124E10D178B CRC64;

Query Match 57.4%; Score 39; DB 16; Length 511;
Best Local Similarity 58.3%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 12
DB 350 CFAWYGLKRV 361

RESULT 8
Q9SWS6

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ID Q9SWS6 PRELIMINARY; PRT; 1121 AA.
AC Q9SWS6;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Phytochrome B2.
GN PHYB2.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; easterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=99413290; PubMed=10485280;
RA  Kerckhoffs L.H., Kelmenson P.M., Schreuder M.E., Kendrick C.I.,
RA  Kendrick R.E., Hanhart C.J., Koornneef M., Pratt L.H.,
RA  Cordonnier-Pratt M.M.;
RT "Characterization of the gene encoding the apoprotein of phytochrome
RT B2 in tomato, and identification of molecular lesions in two mutant
RT alleles.";
RL Mol. Gen. Genet. 261:901-907(1999).
DR EMBL; AF122901; AAD50631.1;
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR003594; ATPBind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR004359; HIS_KIN_sig.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS domain.
DR InterPro; IPR001294; Phytochrome.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF00360; phytochrome; 1.
DR Pfam; PF00512; signal; 1.
DR PRINTS; PR01033; PHYTOCHROME.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HISKA; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR TIGRFAMs; TIGR00229; sensory box; 2.
DR PROSITE; PS00061; ADH SHORT; UNKNOWN_1.
DR PROSITE; PS00245; PHYTOCHROME_1; 1.
DR PROSITE; PS50046; PHYTOCHROME_2; 1.
SQ SEQUENCE 1121 AA; 125308 MW; ED9EDA704BE37F27 CRC64;

Query Match 57.4%; Score 39; DB 10; Length 1121;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFAWQRMKRV 11
DB 777 CFEWNTAMEKL 787

RESULT 9
Q87054 PRELIMINARY; PRT; 134 AA.
ID Q87054;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
DE Z50F protein.
GN Z50F.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RN  SEQUENCE FROM N.A.
RP STRAIN=Z17561;
RA Fallarino A.;

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```
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ231110; CAA13152.1; -. B340DBC6554BFAB CRC64;
SQ SEQUENCE 134 AA; 15496 MW; 1; Mismatches 3; Indels 0; Gaps 0;

Query Match 55.9%; Score 38; DB 2; Length 134;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FAWQAMRKVR 12
DB 7 FAWRALRLKR 17

RESULT 10
Q9C6N2 PRELIMINARY; PRT; 289 AA.
AC Q9C6N2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 33.3 kDa protein.
GN F28L5.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Krenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
DR EMBL: AC079280; AAG50577.1; -.
KW Hypothetical protein.
SQ SEQUENCE 289 AA; 33338 MW; 753AA27BBD0F840C CRC64;

Query Match 55.9%; Score 38; DB 10; Length 289;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFACQAMRKVR 12
DB 8 CFTWBYARHVR 19

RESULT 11
Q98GW4 PRELIMINARY; PRT; 329 AA.
AC Q98GW4;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Membrane lipoprotein.
GN MLR3148.
OS Rhizobium loti (Mesorhizobium loti).
```

```
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL: AP003001; BA850102.1; -.
DR InterPro; IPR003760; Bmp.
DR Pfam; PF02608; Bmp; 1.
KW Lipoprotein; Complete proteome.
SQ SEQUENCE 329 AA; 34754 MW; 78FC399867F6F3D2 CRC64;

Query Match 55.9%; Score 38; DB 16; Length 329;
Best Local Similarity 60.0%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FAWQAMRKV 11
DB 89 FAWEDALKV 98

RESULT 12
Q9KKX6 PRELIMINARY; PRT; 561 AA.
AC Q9KKX6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Methyl-accepting chemotaxis protein.
GN VCA0974.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR Ni6961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL: AE004423; AAF96870.1; -.
DR HSSP; P02942; 1QU7.
DR TIGR; VCA0974; -.
DR InterPro; IPR004089; Chmtaxis_trans.
DR InterPro; IPR003660; HAMP.
DR InterPro; IPR004090; Me_Chemotaxis.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR PRINTS; PR00260; CHEMTNSDUCR.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; NA; 1.
KW Complete proteome.
SQ SEQUENCE 561 AA; 61113 MW; DDA599779A00D64 CRC64;

Query Match 55.9%; Score 38; DB 16; Length 561;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
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Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FAWORAMKVR 12
Db 7 FAWRALELKR 17

RESULT 13

Q9BVH6 PRELIMINARY; PRT; 759 AA.
AC Q9BVH6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 84.7 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DDJ databases.
DR EMBL; BC001202; AA01202.1; -
DR InterPro; IPR003347; TF_JmJC.
DR Pfam; PF02373; jmjC; 1.
KW Hypothetical protein.
SQ SEQUENCE 759 AA; 84712 MW; 5A13F19C0EE952EF CRC64;

Query Match 55.9%; Score 38; DB 4; Length 759;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AWORAMKVR 12
Db 17 AWRAVRGVR 26

RESULT 14

Q9P2G7 PRELIMINARY; PRT; 1265 AA.
AC Q9P2G7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KIAA1380 protein (Fragment).
GN KIAA1380.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;
RT Prediction of the coding sequences of unidentified human genes.XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro.;
RL DNA Res. 7:65-73(2000).
DR EMBL; AB037801; BAA92618.1; -
DR InterPro; IPR003347; TF_JmJC.
DR Pfam; PF02373; jmjC; 1.
FT NON_TER 1
SQ SEQUENCE 1265 AA; 141291 MW; 33DB5BE53A7D9EBE CRC64;

Query Match 55.9%; Score 38; DB 4; Length 1265;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AWORAMKVR 12
Db 17 AWRAVRGVR 26

Db 560 AMKRAVRGVR 569

RESULT 15

Q9NYF4 PRELIMINARY; PRT; 1417 AA.
AC Q9NYF4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative zinc finger protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RX MEDLINE=20541717; PubMed=11087669;
RA Lai F., Godley L.A., Fernald A.A., Orelli B.J., Pamintuan L., Zhao N.,
RA Le Beau M.W.;
RT "cDNA Cloning and Genomic Structure of Three Genes Localized to Human
RT Chromosome Band 5q31 Encoding Potential Nuclear Proteins.";
RL Genomics 70:123-130(2000).
DR EMBL; AF251039; AAF63765.1; -
DR InterPro; IPR003347; TF_JmJC.
DR Pfam; PF02373; jmjC; 1.
SQ SEQUENCE 1417 AA; 154720 MW; E9CF503D8654FD2B CRC64;

Query Match 55.9%; Score 38; DB 4; Length 1417;
Best Local Similarity 70.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AWORAMKVR 12
Db 675 AMKRAVRGVR 684

Search completed: February 21, 2003, 08:00:48
Job time : 22.6744 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:37:21 ; Search time 28.093 Seconds
(without alignments)
56.918 Million cell updates/sec

Title: US-09-743-107b-96

Perfect score: 64

Sequence: 1 CPQLKKNMKKYR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	93.8	12	21	AA198096
2	54	84.4	12	21	AA198080
3	52	81.2	12	21	AA198091
4	52	81.2	12	21	AA198092
5	51	79.7	12	21	AA198081
6	51	79.7	12	21	AA198083
7	50	78.1	12	21	AA198097
8	49	76.6	12	21	AA198071
9	48	75.0	12	21	AA198038
10	48	75.0	12	21	AA198046

11	48	75.0	12	21	AA198047	Human lactoferrin
12	48	75.0	12	21	AA198084	Human lactoferrin
13	48	75.0	13	21	AA198037	Human lactoferrin
14	48	75.0	13	21	AA198048	Human lactoferrin
15	48	75.0	13	21	AA198049	Human lactoferrin
16	48	75.0	14	21	AA198036	Human lactoferrin
17	48	75.0	14	21	AA198050	Human lactoferrin
18	48	75.0	14	21	AA198051	Human lactoferrin
19	48	75.0	15	17	AA198554	Peptide for anti-u
20	48	75.0	15	17	AA198035	Human lactoferrin
21	48	75.0	15	21	AA198062	Human lactoferrin
22	48	75.0	15	21	AA198063	Human lactoferrin
23	48	75.0	16	21	AA198031	Human lactoferrin
24	48	75.0	16	21	AA198064	Human lactoferrin
25	48	75.0	16	21	AA198065	Human lactoferrin
26	48	75.0	17	21	AA198034	Human lactoferrin
27	48	75.0	17	21	AA198066	Human lactoferrin
28	48	75.0	17	21	AA198067	Human lactoferrin
29	48	75.0	17	21	AA198352	Human lactoferrin
30	48	75.0	18	17	AA193397	Advanced glycosyla
31	48	75.0	18	21	AA198033	Human lactoferrin
32	48	75.0	19	21	AA198867	Amino acid sequen
33	48	75.0	19	21	AA198032	Human lactoferrin
34	48	75.0	20	13	AA1921810	Anti microbial pep
35	48	75.0	20	14	AA194841	Lactoferrin-rlate
36	48	75.0	20	15	AA1948530	Lactoferrin derive
37	48	75.0	20	15	AA1948531	Lactoferrin derive
38	48	75.0	20	15	AA1957461	Lactoferrin derive
39	48	75.0	20	15	AA1957462	Lactoferrin derive
40	48	75.0	20	16	AA1984698	Bovine lactoferrin
41	48	75.0	20	16	AA1984699	Bovine lactoferrin
42	48	75.0	20	16	AA1980263	Anti-parasitic lac
43	48	75.0	20	16	AA1980264	Anti-parasitic lac
44	48	75.0	20	17	AA198553	Peptide for anti-u
45	48	75.0	20	17	AA191852	Lactoferrin-derive

ALIGNMENTS

RESULT 1
AA198096
ID AA198096 standard; Peptide; 12 AA.
XX
AC AA198096;
XX
DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:96.

Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.

XX Homo sapiens.
OS Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

PR 17-JUL-1998; 98SE-0002562.

PR 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

DR WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -
XX
PS Claim 22; Page 36; 102pp; English.
XX
CC AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.
XX
SQ Sequence 12 AA;
Query Match 93.8%; Score 60; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00059;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFOLKKNKKVR 12
DB 1 CFOLKKNKKVR 12
RESULT 2
AAY78080
ID AAY78080 standard; Peptide; 12 AA.
AC AAY78080;
XX
XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:80.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200001730-A1.
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCII-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
XX inflammations and tumors and for use in infant formula food -
XX
XX Claim 22; Page 36; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
XX lactoferrin. The peptides are taken up in the intestine through
XX binding to specific lactoferrin receptors and are then transported
XX through the circulation. A medicinal product of the peptide or fragment
XX can be used for treating and/or prevention of infections (such as
XX urinary tract infections, colitis, and Candida infection on a mucosal
XX membrane), inflammations and/or tumours. The peptides can also be used
XX in food stuffs such as infant formula food. The peptides are also
XX fungicidal and bactericidal and may also be used as preservatives.
XX Even though native human lactoferrin have been shown to have desired
XX anti-inflammatory anti-infectious and anti-tumoural properties they
XX cannot be used clinically on a broad basis because of high production
XX costs. Therefore, provision of peptides based on lactoferrin would
XX enable them to be used for the same purposes as lactoferrin at lower
XX cost.
XX
SQ Sequence 12 AA;
Query Match 84.4%; Score 54; DB 21; Length 12;
Best Local Similarity 75.0%; Pred. No. 0.0066;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFOLKKNKKVR 12
DB 1 CFOLKKNKKVR 12
RESULT 3
AAY78091
ID AAY78091 standard; Peptide; 12 AA.
AC AAY78091;
XX
XX 25-APR-2000 (first entry)
XX Human lactoferrin derived peptide SEQ ID NO:91.
XX
XX Human; lactoferrin; modification; infection; inflammation; tumour;
XX food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX urinary tract infection; colitis; Candida infection; fungicidal;
XX bactericidal; preservative.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200001730-A1.
XX 13-JAN-2000.
XX
XX 06-JUL-1999; 99WO-SE01230.
XX
XX 06-JUL-1998; 98SE-0002441.
XX 17-JUL-1998; 98SE-0002562.
XX 29-DEC-1998; 98SE-0004614.
XX
XX (ASCII-) A+ SCI INVEST AB.
XX
XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX
XX New peptides used for treatment and prevention of infections,
XX inflammations and tumors and for use in infant formula food -
XX
XX Claim 22; Page 38; 102pp; English.
XX
XX AAY78001 to AAY78100 represent peptides having sequences based on human
XX lactoferrin. The peptides are taken up in the intestine through
XX binding to specific lactoferrin receptors and are then transported
XX through the circulation. A medicinal product of the peptide or fragment
XX can be used for treating and/or prevention of infections (such as
XX urinary tract infections, colitis, and Candida infection on a mucosal
XX membrane), inflammations and/or tumours. The peptides can also be used
XX in food stuffs such as infant formula food. The peptides are also

CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 81.2%; Score 52; DB 21; Length 12;
 Best Local Similarity 75.0%; Pred. No. 0.015;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQLKKNKKVR 12
 ||| |.:|:|
 Db 1 CFQWKNNKKVR 12

RESULT 4
 AAY78092
 ID AAY78092 standard; Peptide; 12 AA.

XX AC AAY78092;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:92.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200001730-A1.
 XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 XX PR 17-JUL-1998; 98SE-0002562.
 XX PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCI-) A+ SCI INVEST AB.
 XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX DR WPI; 2000-147388/13.

XX FT New peptides used for treatment and prevention of infections,
 XX PT inflammations and tumors and for use in infant formula food -
 XX PS Claim 22; Page 38; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;
 Query Match 81.2%; Score 52; DB 21; Length 12;
 Best Local Similarity 75.0%; Pred. No. 0.015;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFQLKKNKKVR 12
 ||| |.:|:|
 Db 1 CFQWKNNKKVR 12

RESULT 5
 AAY78081
 ID AAY78081 standard; Peptide; 12 AA.

XX AC AAY78081;
 XX DT 25-APR-2000 (first entry)
 XX DE Human lactoferrin derived peptide SEQ ID NO:81.
 XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
 XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 XX KW urinary tract infection; colitis; Candida infection; fungicidal;
 XX KW bactericidal; preservative.

XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200001730-A1.
 XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.
 XX PR 06-JUL-1998; 98SE-0002441.
 XX PR 17-JUL-1998; 98SE-0002562.
 XX PR 29-DEC-1998; 98SE-0004614.
 XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 XX DR WPI; 2000-147388/13.

XX FT New peptides used for treatment and prevention of infections,
 XX PT inflammations and tumors and for use in infant formula food -
 XX PS Claim 22; Page 36; 102pp; English.

XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 12 AA;

Query Match 79.7%; Score 51; DB 21; Length 12;
 Best Local Similarity 75.0%; Pred. No. 0.022;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOLKKNKKVR 12
 DB 1 CFQWQKNKKVR 12

RESULT 6

AA78083
 ID AAY78083 standard; Peptide; 12 AA.

XX
 AC AAY78083;

XX
 DT 25-APR-2000 (first entry)

XX
 DE Human lactoferrin derived peptide SEQ ID NO:83.

XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX
 OS Homo sapiens.
 OS Synthetic.

XX
 PN WO200001730-A1.

XX
 PD 13-JAN-2000.

XX
 PF 06-JUL-1999; 99WO-SE01230.

XX
 PR 06-JUL-1998; 98SE-0002441.

XX
 PR 17-JUL-1998; 98SE-0002562.

XX
 PR 29-DEC-1998; 98SE-0004614.

XX
 PA (ASCI-) A+ SCI INVEST AB.

XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX
 DR WPI; 2000-147388/13.

XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX
 PS Claim 22; Page 36; 102pp; English.

XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX
 SQ Sequence 12 AA;

Query Match 79.7%; Score 51; DB 21; Length 12;

Best Local Similarity 75.0%; Pred. No. 0.022; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOLKKNKKVR 12
 DB 1 CFQWQKNKKVR 12

RESULT 7

AA78097

ID AAY78097 standard; Peptide; 12 AA.

XX
 AC AAY78097;

XX
 DT 25-APR-2000 (first entry)

XX
 DE Human lactoferrin derived peptide SEQ ID NO:97.

XX
 KW Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.

XX
 OS Homo sapiens.
 OS Synthetic.

XX
 PN WO200001730-A1.

XX
 PD 13-JAN-2000.

XX
 PF 06-JUL-1999; 99WO-SE01230.

XX
 PR 06-JUL-1998; 98SE-0002441.

XX
 PR 17-JUL-1998; 98SE-0002562.

XX
 PR 29-DEC-1998; 98SE-0004614.

XX
 PA (ASCI-) A+ SCI INVEST AB.

XX
 PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX
 DR WPI; 2000-147388/13.

XX
 PT New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -

XX
 PS Claim 19; Page 94; 102pp; English.

XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumors. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX
 SQ Sequence 12 AA;

Query Match 78.1%; Score 50; DB 21; Length 12;

Best Local Similarity 83.3%; Pred. No. 0.033; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOLKKNKKVR 12
 DB 1 CFALKKKKKKVR 12

RESULT 8

AA78071

ID AAY78071 standard; Peptide; 12 AA.

XX
 AC AAY78071;

XX
 DT 25-APR-2000 (first entry)

XX
 DE Human lactoferrin derived peptide SEQ ID NO:71.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 XX 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 XX
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 XX
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT
 PS Claim 22; Page 35; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 76.6%; Score 49; DB 21; Length 12;
 Best Local Similarity 66.7%; Pred. No. 0.049;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQLKKNMKKVR 12
 DB 1 CFQQRNMRKVR 12
 RESULT 9
 AAY78038
 ID AAY78038 standard; Peptide; 12 AA.
 XX
 XX AAY78038;
 AC
 XX 25-APR-2000 (first entry)
 DT
 XX Human lactoferrin derived peptide SEQ ID NO:38.
 DE
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.

OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 PF
 XX 06-JUL-1998; 98SE-0002441.
 PR 17-JUL-1998; 98SE-0002562.
 PR 29-DEC-1998; 98SE-0004614.
 XX
 XX (ASCI-) A+ SCI INVEST AB.
 PA
 XX Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
 PI WPI; 2000-147388/13.
 XX
 XX New peptides used for treatment and prevention of infections,
 PT inflammations and tumors and for use in infant formula food -
 PT
 PS Claim 12; Page 70; 102pp; English.
 XX
 CC AAY78001 to AAY78100 represent peptides having sequences based on human
 CC lactoferrin. The peptides are taken up in the intestine through
 CC binding to specific lactoferrin receptors and are then transported
 CC through the circulation. A medicinal product of the peptide or fragment
 CC can be used for treating and/or prevention of infections (such as
 CC urinary tract infections, colitis, and Candida infection on a mucosal
 CC membrane), inflammations and/or tumours. The peptides can also be used
 CC in food stuffs such as infant formula food. The peptides are also
 CC fungicidal and bactericidal and may also be used as preservatives.
 CC Even though native human lactoferrin have been shown to have desired
 CC anti-inflammatory anti-infectious and anti-tumoural properties they
 CC cannot be used clinically on a broad basis because of high production
 CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 75.0%; Score 48; DB 21; Length 12;
 Best Local Similarity 66.7%; Pred. No. 0.073;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CFQLKKNMKKVR 12
 DB 1 CFQQRNMRKVR 12
 RESULT 10
 AAY78046
 ID AAY78046 standard; Peptide; 12 AA.
 XX
 XX AAY78046;
 AC
 XX 25-APR-2000 (first entry)
 DT
 XX Human lactoferrin derived peptide SEQ ID NO:46.
 DE
 XX Human; lactoferrin; modification; infection; inflammation; tumour;
 KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
 KW urinary tract infection; colitis; Candida infection; fungicidal;
 KW bactericidal; preservative.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001730-A1.
 XX
 PD 13-JAN-2000.
 XX
 XX 06-JUL-1999; 99WO-SE01230.
 PF

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XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX DR WPI; 2000-147388/13.
XX XX
XX PT New peptides used for treatment and prevention of infections,
XX PT inflammations and tumors and for use in infant formula food -
XX PS Claim 15; Page 35; 102pp; English.
XX XX
XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
XX CC lactoferrin. The peptides are taken up in the intestine through
XX CC binding to specific lactoferrin receptors and are then transported
XX CC through the circulation. A medicinal product of the peptide or fragment
XX CC can be used for treating and/or prevention of infections (such as
XX CC urinary tract infections, colitis, and Candida infection on a mucosal
XX CC membrane), inflammations and/or tumours. The peptides can also be used
XX CC in food stuffs such as infant formula food. The peptides are also
XX CC fungicidal and bactericidal and may also be used as preservatives.
XX CC Even though native human lactoferrin have been shown to have desired
XX CC anti-inflammatory anti-infectious and anti-tumoural properties they
XX CC cannot be used clinically on a broad basis because of high production
XX CC costs. Therefore, provision of peptides based on lactoferrin would
XX CC enable them to be used for the same purposes as lactoferrin at lower
XX CC cost.
XX SQ Sequence 12 AA;
XX Query Match 75.0%; Score 48; DB 21; Length 12;
XX Best Local Similarity 66.7%; Pred. No. 0.073; 1; Indels 0; Gaps 0;
XX Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQLKKNMKVVR 12
DB ||| :|||:
1 CFQWQNNMKVVR 12

RESULT 11
AAY78047
ID AAY78047 standard; Peptide; 12 AA.
XX AC AAY78047;
XX DT 25-APR-2000 (first entry)
XX DE Human lactoferrin derived peptide SEQ ID NO:47.
XX XX
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX PN WO200001730-A1.
XX XX
XX PD 13-JAN-2000.
XX XX
XX PF 06-JUL-1999; 99WO-SE01230.
XX XX
XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX DR WPI; 2000-147388/13.
XX XX
XX PT New peptides used for treatment and prevention of infections,
XX PT inflammations and tumors and for use in infant formula food -

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PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX WPI; 2000-147388/13.
XX XX
XX PT New peptides used for treatment and prevention of infections,
XX PT inflammations and tumors and for use in infant formula food -
XX PS Claim 18; Page 73; 102pp; English.
XX XX
XX CC AAY78001 to AAY78100 represent peptides having sequences based on human
XX CC lactoferrin. The peptides are taken up in the intestine through
XX CC binding to specific lactoferrin receptors and are then transported
XX CC through the circulation. A medicinal product of the peptide or fragment
XX CC can be used for treating and/or prevention of infections (such as
XX CC urinary tract infections, colitis, and Candida infection on a mucosal
XX CC membrane), inflammations and/or tumours. The peptides can also be used
XX CC in food stuffs such as infant formula food. The peptides are also
XX CC fungicidal and bactericidal and may also be used as preservatives.
XX CC Even though native human lactoferrin have been shown to have desired
XX CC anti-inflammatory anti-infectious and anti-tumoural properties they
XX CC cannot be used clinically on a broad basis because of high production
XX CC costs. Therefore, provision of peptides based on lactoferrin would
XX CC enable them to be used for the same purposes as lactoferrin at lower
XX CC cost.
XX SQ Sequence 12 AA;
XX Query Match 75.0%; Score 48; DB 21; Length 12;
XX Best Local Similarity 66.7%; Pred. No. 0.073; 1; Indels 0; Gaps 0;
XX Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQLKKNMKVVR 12
DB ||| :|||:
1 CFQWQNNMKVVR 12

RESULT 12
AAY78084
ID AAY78084 standard; Peptide; 12 AA.
XX AC AAY78084;
XX DT 25-APR-2000 (first entry)
XX DE Human lactoferrin derived peptide SEQ ID NO:84.
XX XX
XX KW Human; lactoferrin; modification; infection; inflammation; tumour;
XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
XX KW urinary tract infection; colitis; Candida infection; fungicidal;
XX KW bactericidal; preservative.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX PN WO200001730-A1.
XX XX
XX PD 13-JAN-2000.
XX XX
XX PF 06-JUL-1999; 99WO-SE01230.
XX XX
XX PR 06-JUL-1998; 98SE-0002441.
XX PR 17-JUL-1998; 98SE-0002562.
XX PR 29-DEC-1998; 98SE-0004614.
XX PA (ASCI-) A+ SCI INVEST AB.
XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
XX DR WPI; 2000-147388/13.
XX XX
XX PT New peptides used for treatment and prevention of infections,
XX PT inflammations and tumors and for use in infant formula food -

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PS Claim 22; Page 36; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX Sequence 12 AA;

Query Match 75.0%; Score 48; DB 21; Length 12;

Best Local Similarity 66.7%; Pred. No. 0.073;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQLKKNMKVVR 12

Db 1 CFQWERNMKVR 12

RESULT 13

AAY78037

ID AAY78037 standard; Peptide; 13 AA.

XX AAY78037;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:37.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -

XX Claim 12; Page 70; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as

CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production
CC costs. Therefore, provision of peptides based on lactoferrin would
CC enable them to be used for the same purposes as lactoferrin at lower
CC cost.

XX Sequence 13 AA;

Query Match 75.0%; Score 48; DB 21; Length 13;

Best Local Similarity 66.7%; Pred. No. 0.079;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQLKKNMKVVR 12

Db 2 CFQWERNMKVR 13

RESULT 14

AAY78048

ID AAY78048 standard; Peptide; 13 AA.

XX AAY78048;

XX 25-APR-2000 (first entry)

XX Human lactoferrin derived peptide SEQ ID NO:48.

XX Human; lactoferrin; modification; infection; inflammation; tumour;
KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
KW urinary tract infection; colitis; Candida infection; fungicidal;
KW bactericidal; preservative.

XX Homo sapiens.

XX Synthetic.

XX WO200001730-A1.

XX 13-JAN-2000.

XX 06-JUL-1999; 99WO-SE01230.

XX 06-JUL-1998; 98SE-0002441.

XX 17-JUL-1998; 98SE-0002562.

XX 29-DEC-1998; 98SE-0004614.

XX (ASCI-) A+ SCI INVEST AB.

XX Hanson LA, Matteby-Baltzer I, Baltzer L, Dolphin GT;

XX WPI; 2000-147388/13.

XX New peptides used for treatment and prevention of infections,
PT inflammations and tumors and for use in infant formula food -

XX Claim 15; Page 74; 102pp; English.

XX AAY78001 to AAY78100 represent peptides having sequences based on human
CC lactoferrin. The peptides are taken up in the intestine through
CC binding to specific lactoferrin receptors and are then transported
CC through the circulation. A medicinal product of the peptide or fragment
CC can be used for treating and/or prevention of infections (such as
CC urinary tract infections, colitis, and Candida infection on a mucosal
CC membrane), inflammations and/or tumours. The peptides can also be used
CC in food stuffs such as infant formula food. The peptides are also
CC fungicidal and bactericidal and may also be used as preservatives.
CC Even though native human lactoferrin have been shown to have desired
CC anti-inflammatory anti-infectious and anti-tumoural properties they
CC cannot be used clinically on a broad basis because of high production

CC costs. Therefore, provision of peptides based on lactoferrin would
 CC enable them to be used for the same purposes as lactoferrin at lower
 CC cost.

XX SQ Sequence 13 AA;

Query Match 75.0%; Score 48; DB 21; Length 13;

Best Local Similarity 66.7%; Pred. No. 0.079;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOLKKNMKVR 12

DB 2 CFQWRNMEKVR 13

RESULT 15

AAV78049

ID AAV78049 standard; Peptide; 13 AA.

XX AC AAV78049;

XX DT 25-APR-2000 (first entry)

XX DE Human lactoferrin derived peptide SEQ ID NO:49.

XX KW Human; lactoferrin; modification; infection; inflammation; tumour;

XX KW food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;

XX KW urinary tract infection; colitis; Candida infection; fungicidal;

XX KW bactericidal; preservative.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001730-A1.

XX PD 13-JAN-2000.

XX PF 06-JUL-1999; 99WO-SE01230.

XX PR 06-JUL-1998; 98SE-0002441.

XX PR 17-JUL-1998; 98SE-0002562.

XX PR 29-DEC-1998; 98SE-0004614.

XX PA (ASCI-) A+ SCI INVEST AB.

XX PI Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

XX DR WPI; 2000-147388/13.

XX PT New peptides used for treatment and prevention of infections,

XX PT inflammations and tumors and for use in infant formula food -

XX PS Claim 18; Page 74; 102pp; English.

XX CC AAV78001 to AAV78100 represent peptides having sequences based on human

XX CC lactoferrin. The peptides are taken up in the intestine through

XX CC binding to specific lactoferrin receptors and are then transported

XX CC through the circulation. A medicinal product of the peptide or fragment

XX CC can be used for treating and/or prevention of infections (such as

XX CC urinary tract infections, colitis, and Candida infection on a mucosal

XX CC membrane), inflammations and/or tumours. The peptides can also be used

XX CC in food stuffs such as infant formula food. The peptides are also

XX CC fungicidal and bactericidal and may also be used as preservatives.

XX CC Even though native human lactoferrin have been shown to have desired

XX CC anti-inflammatory anti-infectious and anti-tumoural properties they

XX CC cannot be used clinically on a broad basis because of high production

XX CC costs. Therefore, provision of peptides based on lactoferrin would

XX CC enable them to be used for the same purposes as lactoferrin at lower

XX CC cost.

XX SQ Sequence 13 AA;

Query Match

75.0%; Score 48; DB 21; Length 13;

Best Local Similarity 66.7%; Pred. No. 0.079;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOLKKNMKVR 12

DB 2 CFQWRNMEKVR 13

Search completed: February 21, 2003, 07:56:45

Job time : 28.093 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 07:50:40, Search time 8.93023 Seconds
(without alignments)
39.537 Million cell updates/sec

Title: US-09-743-107B-96
Perfect score: 64
Sequence: 1 CFOLKKNMKVR 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/prodata/1/aaa/5A_COMB.psp:
2: /cgn2_6/prodata/1/aaa/5B_COMB.psp:
3: /cgn2_6/prodata/1/aaa/6A_COMB.psp:
4: /cgn2_6/prodata/1/aaa/6B_COMB.psp:
5: /cgn2_6/prodata/1/aaa/PCUS_COMB.psp:
6: /cgn2_6/prodata/1/aaa/backfiles1.psp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	75.0	18	1	US-08-204-487-3
2	48	75.0	18	2	US-08-485-948-8
3	48	75.0	18	2	US-08-628-380-8
4	48	75.0	18	2	US-08-475-055-8
5	48	75.0	20	1	US-07-753-161A-3
6	48	75.0	20	1	US-07-891-174-3
7	48	75.0	20	1	US-08-204-487-1
8	48	75.0	20	1	US-08-256-771-24
9	48	75.0	20	1	US-08-256-771-25
10	48	75.0	20	1	US-08-381-984-24
11	48	75.0	20	1	US-08-381-984-25
12	48	75.0	22	4	US-09-508-734-4
13	48	75.0	24	4	US-09-508-734-6
14	48	75.0	25	1	US-07-755-161A-10
15	48	75.0	25	1	US-07-891-174-10
16	48	75.0	25	1	US-08-204-487-7
17	48	75.0	29	4	US-09-508-734-8
18	48	75.0	36	1	US-07-753-161A-8
19	48	75.0	36	1	US-07-891-174-8
20	48	75.0	36	1	US-08-256-771-30
21	48	75.0	36	1	US-08-381-984-29
22	48	75.0	47	2	US-08-464-182A-6
23	48	75.0	47	2	US-08-406-271-6
24	48	75.0	50	2	US-08-693-274A-7
25	48	75.0	52	4	US-09-011-043A-3
26	48	75.0	53	2	US-08-464-182A-5
27	48	75.0	53	2	US-08-406-271-5

28	48	75.0	54	2	US-08-464-182A-2	Sequence 2, Appli
29	48	75.0	54	2	US-08-406-271-2	Sequence 2, Appli
30	48	75.0	694	3	US-08-724-586-2	Sequence 2, Appli
31	48	75.0	694	4	US-09-421-632-2	Sequence 2, Appli
32	48	75.0	694	4	US-09-932-190-2	Sequence 2, Appli
33	48	75.0	705	2	US-08-655-640-2	Sequence 2, Appli
34	48	75.0	708	2	US-08-655-640-4	Sequence 4, Appli
35	48	75.0	711	1	US-08-154-019-4	Sequence 4, Appli
36	48	75.0	711	1	US-08-461-333-4	Sequence 4, Appli
37	48	75.0	711	3	US-08-464-167-4	Sequence 4, Appli
38	48	75.0	711	3	US-09-158-313-4	Sequence 4, Appli
39	48	75.0	711	4	US-08-475-798-4	Sequence 4, Appli
40	45	70.3	711	1	US-08-145-681-2	Sequence 2, Appli
41	45	70.3	711	1	US-08-250-308-2	Sequence 2, Appli
42	45	70.3	711	1	US-08-453-703-2	Sequence 2, Appli
43	45	70.3	711	2	US-08-456-106-2	Sequence 2, Appli
44	45	70.3	711	3	US-08-456-108-2	Sequence 2, Appli
45	45	70.3	711	4	US-09-265-577-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-487-3
; Sequence 3, Application US/082044487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGEAKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FCN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE"

OTHER INFORMATION: (20-37)"
US-08-204-487-3

Query Match 75.0%; Score 48; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.056;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFOLKKNMKVR 12
||| :||:|
Db 1 CFQWRNMRKVR 12

RESULT 2

US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5835882
; GENERAL INFORMATION:
; APPLICANT: YONG MING LI
; APPLICANT: HELEN VLASSARA
; APPLICANT: ANTHONY CERAMI
; TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
FILING DATE: APRIL 7, 1995

CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-Cl, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

US-08-485-948-8

Query Match 75.0%; Score 48; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.056;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFOLKKNMKVR 12
||| :||:|
Db 1 CFQWRNMRKVR 12

RESULT 3

US-08-628-380-8
; Sequence 8, Application US/08628380
; Patent No. 5891341
; GENERAL INFORMATION:
; APPLICANT: LI, YONG MING
; APPLICANT: VLASSARA, HELEN
; APPLICANT: CERAMI, ANTHONY
; TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-Cl, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

US-08-628-380-8

Query Match 75.0%; Score 48; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.056;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFOLKKNMKVR 12
||| :||:|
Db 1 CFQWRNMRKVR 12

RESULT 4

US-08-475-055-8
; Sequence 8, Application US/08475055
; Patent No. 5962245
; GENERAL INFORMATION:

APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-CI, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8

Query Match 75.0%; Score 48; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.056;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQLKKNMKVR 12
Db 1 CFQQRNMRKV 12

RESULT 5
US-07-755-161A-3
Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
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OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755.161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3

Query Match 75.0%; Score 48; DB 1; Length 20;
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Best Local Similarity 65.7%; Pred. No. 0.062;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOLKKNMKVR 12
DB 2 CFQWRNMRKVR 13

RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Displaywrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHEICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site

LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3

Query Match 75.0%; Score 48; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 0.062;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOLKKNMKVR 12
DB 2 CFQWRNMRKVR 13

RESULT 7
US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NAOKI
; APPLICANT: NAKASHIMA, HIDEKI
; APPLICANT: MOSUCHI, WATARU
; APPLICANT: TANAKA, SHIGERAKI
; APPLICANT: DOSAKO, SHUN'ICHI
; APPLICANT: KAWASAKI, YOSHIHIRO
; APPLICANT: UCHIDA, TOSHIAKI
; TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,487
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FUN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE"
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1

Query Match 75.0%; Score 48; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 0.062;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQLKKNMKVR 12
|||:|:|:|
Db 2 CFQWRNMRKVR 13

RESULT 8
US-08-256-771-24
; Sequence 24, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"

Query Match 75.0%; Score 48; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 0.062;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQLKKNMKVR 12
|||:|:|:|
Db 2 CFQWRNMRKVR 13

RESULT 10
US-08-381-984-24

US-08-256-771-24

Query Match 75.0%; Score 48; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 0.062;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQLKKNMKVR 12
|||:|:|:|
Db 2 CFQWRNMRKVR 13

RESULT 9
US-08-256-771-25
; Sequence 25, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to
OTHER INFORMATION: prevent disulfide bond"

US-08-256-771-25
Query Match 75.0%; Score 48; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 0.062;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQLKKNMKVR 12
|||:|:|:|
Db 2 CFQWRNMRKVR 13

RESULT 10
US-08-381-984-24

Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-24
Query Match 75.0%; Score 48; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 0.062;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFWQKNNMKVVR 12
DB 2 CFWQKNNMKVVR 13
RESULT 11
US-08-381-984-25
Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-25
Query Match 75.0%; Score 48; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 0.062;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 CFWQKNNMKVVR 12
DB 2 CFWQKNNMKVVR 13
RESULT 12
US-09-508-734-4
Sequence 4, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4

```
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
IS-09-508-734-4
Query Match 75.0%; Score 48; DB 4; Length 22;
Best Local Similarity 66.7%; Pred. No. 0.068;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

y 1 CFOLKKNMKVR 12
   ||| :|||
   ||| :|||
b 2 CFQWRNMRKVR 13

RESULT 13
IS-09-508-734-6
Sequence 6, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: KopatentIn 1.71
SEQ ID NO 6
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
IS-09-508-734-6
Query Match 75.0%; Score 48; DB 4; Length 24;
Best Local Similarity 66.7%; Pred. No. 0.074;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

y 1 CFOLKKNMKVR 12
   ||| :|||
   ||| :|||
b 3 CFQWRNMRKVR 14

RESULT 14
IS-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
FILE REFERENCE: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
NAME/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
Query Match 75.0%; Score 48; DB 1; Length 25;
Best Local Similarity 66.7%; Pred. No. 0.077;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CFOLKKNMKVR 12
   ||| :|||
   ||| :|||
Db 4 CFQWRNMRKVR 15
```

RESULT 15

US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptides and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,174
; FILING DATE: 29-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,161
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 4
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 21"
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 21

; IDENTIFICATION METHOD:

; OTHER INFORMATION: /note= "thiol group of
; OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
; OTHER INFORMATION: thiol group of Cys residue at location 4"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-891-174-10
; Query Match 75.0%; Score 48; DB 1; Length 25;
; Best Local Similarity 66.7%; Pred. NO. 0.077;
; Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
; Qy 1 CFOLKXNMKKVR 12
; Db 4 CFOWQRMKKVR 15
; Search completed: February 21, 2003, 08:04:28
; Job time : 9.93023 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 08:08:15 ; Search time 6.88372 Seconds
(without alignments)
54.162 Million cell updates/sec

Title: US-09-743-107B-96

Perfect score: 64

Sequence: 1 CFOLKKMKVKVR 12

Scoring table: Gapox 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep.*
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 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW PUB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	75.0	15	9	US-09-798-869-2
2	48	75.0	25	9	US-09-798-869-20
3	48	75.0	694	9	US-10-023-096-2
4	43	67.2	15	9	US-09-798-869-6
5	42	65.6	351	10	US-09-853-625B-16
6	39	60.9	57	10	US-09-864-761-37163
7	37	57.8	28	9	US-09-974-879-345
8	37	57.8	784	10	US-09-905-983-52
9	36	56.2	358	10	US-09-841-132-539
10	36	56.2	358	12	US-10-007-693-107
11	35	54.7	46	10	US-09-864-761-43420
12	35	54.7	373	10	US-09-760-354A-2
13	34	53.1	347	10	US-09-851-588-4
14	34	53.1	371	9	US-10-046-935-2235
15	34	53.1	371	9	US-09-878-178-2235
16	34	53.1	391	9	US-10-046-935-2239
17	34	53.1	407	10	US-09-925-301-1165
18	33	51.6	35	10	US-09-764-877-1302
19	33	51.6	48	10	US-09-864-761-40172

20	33	51.6	48	10	US-09-071-838-202
21	33	51.6	54	10	US-09-764-846-244
22	33	51.6	65	10	US-09-864-761-42127
23	33	51.6	116	10	US-09-764-853-738
24	33	51.6	193	9	US-09-796-692-2458
25	33	51.6	329	10	US-09-927-738-11
26	33	51.6	333	10	US-09-765-272-58
27	33	51.6	336	9	US-09-987-107-33
28	33	51.6	336	10	US-09-800-729-207
29	33	51.6	401	9	US-09-987-107-36
30	33	51.6	429	9	US-09-987-107-34
31	33	51.6	470	10	US-09-861-451A-14
32	33	51.6	1499	10	US-09-911-836A-2
33	32	50.0	75	9	US-09-981-876-172
34	32	50.0	75	9	US-09-148-543-172
35	32	50.0	152	9	US-09-738-626-5856
36	32	50.0	184	10	US-09-925-301-1248
37	32	50.0	243	10	US-09-815-242-10838
38	32	50.0	347	10	US-09-815-242-11530
39	32	50.0	391	9	US-09-987-107-38
40	32	50.0	391	10	US-09-800-729-208
41	32	50.0	395	9	US-09-987-107-35
42	32	50.0	447	9	US-10-155-789-4
43	32	50.0	447	9	US-10-155-789-17
44	32	50.0	447	12	US-10-042-417-10
45	32	50.0	448	10	US-09-866-562-37

ALIGNMENTS

RESULT 1
US-09-798-869-2
; Sequence 2, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON
; APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2
Query Match 75.0%; Score 48; DB 9; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.04;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CFOLKKMKVKVR 12
Db 3 CFQWRNRKVR 14
RESULT 2
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: BALDUR SVEINBJ (RNSON

APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-798-869-20

Query Match 75.0%; Score 48; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 0.065;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOLKKNKKVR 12
DB 3 CFQWQNRKVR 14

RESULT 3

US-10-023-096-2
Sequence 2, Application US/10023096
Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA: US/08/724,586
APPLICATION NUMBER: 31,409
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-023-096-2

Query Match 75.0%; Score 48; DB 9; Length 694;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOLKKNKKVR 12
DB 22 CFQWQNRKVR 33

RESULT 4

US-09-798-869-6
Sequence 6, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJARNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
OTHER INFORMATION: sequence)
US-09-798-869-6

Query Match 67.2%; Score 43; DB 9; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.26;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOLKKNKKVR 12
DB 3 CFQWQNRKVR 14

RESULT 5

US-09-853-625B-16
Sequence 16, Application US/09853625B
Patent No. US20020049304A1
GENERAL INFORMATION:
APPLICANT: Hastings, Gregg A. and Adams, Mark D.
TITLE OF INVENTION: Human CCN-Like Growth Factor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/853,625B
FILING DATE: 14-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/053,587

FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33,073
 REFERENCE/DOCKET NUMBER: 325800-442
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 351 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS: <Unknown>
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 S-09-853-625B-16

Query Match 65.6%; Score 42; DB 10; Length 351;
 Best Local Similarity 66.7%; Pred. No. 7.7;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Y 1 CFOLKKNMKV 12
 |||||
 b 258 CIQTKSKAVR 269

RESULT 6
 US-09-864-761-37163
 Sequence 37163, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aconica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 37163
 LENGTH: 57
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL022169.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.2
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.2
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.4
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 10
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 10
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.5
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.7
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.7
 OTHER INFORMATION: EST HUMAN HIT: AW974650.1, EVALUATE 1.00e-26
 OTHER INFORMATION: SWISSPROT HIT: O07920, EVALUATE 2.60e+00
 US-09-864-761-37163

Query Match 60.9%; Score 39; DB 10; Length 57;
 Best Local Similarity 60.0%; Pred. No. 4.2;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOLKKNMKK 10
 |||||
 Db 47 CFSLSKNLKR 56

RESULT 7
 US-09-974-879-345
 Sequence 345, Application US/09974879
 Publication No. US20030028003A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 125 Human Secreted Proteins
 FILE REFERENCE: P20202
 CURRENT APPLICATION NUMBER: US/09/974,879
 CURRENT FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: US 60/239,893
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: US 09/818,683
 PRIOR FILING DATE: 2001-03-28
 PRIOR APPLICATION NUMBER: US 09/305,736
 PRIOR FILING DATE: 1999-05-05
 PRIOR APPLICATION NUMBER: PCT/US98/23435
 PRIOR FILING DATE: 1998-11-04
 PRIOR APPLICATION NUMBER: US 60/064,911
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: US 60/064,912
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: US 60/064,983
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: US 60/064,900
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: US 60/064,988
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: US 60/064,987
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: US 60/064,908
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: US 60/064,984
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: US 60/064,985
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: US 60/066,094
 PRIOR FILING DATE: 1997-11-17

```

US-09-841-132-599
Query Match 56.2%; Score 36; DB 10; Length 358;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOLKKNMKX 10
| | | | |
DB 251 CYVLKKNMKX 260

RESULT 10
US-10-007-693-107
; Sequence 107, Application US/10007693
; Patent No. US20020146776A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.515C2
; CURRENT APPLICATION NUMBER: US/10/007,693
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 107
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis serovar D
US-10-007-693-107

Query Match 56.2%; Score 36; DB 12; Length 358;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOLKKNMKX 10
| | | | |
DB 251 CYVLKKNMKX 260

RESULT 11
US-09-864-761-43420
; Sequence 43420, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

US-09-841-132-599
Query Match 57.8%; Score 37; DB 9; Length 28;
Best Local Similarity 80.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 OLKKNMKYR 12
| | | | |
DB 10 OLKKNMKYR 19

RESULT 8
US-09-905-983-52
; Sequence 52, Application US/09905983
; Patent No. US20020045591A1
; GENERAL INFORMATION:
; APPLICANT: Geiger, Benjamin
; APPLICANT: Ben-Ze'ev, Avri
; APPLICANT: Sadot, Einat
; TITLE OF INVENTION: METHODS AND THERAPEUTIC COMPOSITIONS FOR TREATING CANCER
; FILE REFERENCE: 01/22326
; CURRENT APPLICATION NUMBER: US/09/905,983
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-983-52

Query Match 57.8%; Score 37; DB 10; Length 784;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 2 FOLKKNMKX 10
| | | | |
DB 379 FOLKKNMKX 387

RESULT 9
US-09-841-132-599
; Sequence 599, Application US/09841132
; Patent No. US20020061849A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 599
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis serovar D

```

PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43420
LENGTH: 46
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004962.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: P05458, EVALU4 4.80e+00

Query Match 54.7%; Score 35; DB 10; Length 46;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
1 CFQLKKNMKV 11
|||
5 CFSKKLMKEV 15

RESULT 12
US-09-760-354A-2
Sequence 2, Application US/09760354A
Patent No. US20020042385A1
GENERAL INFORMATION:
APPLICANT: Bergsma, Derek S.
APPLICANT: Shabon, Usman
APPLICANT: Elshourbasy, Nabil
TITLE OF INVENTION: CLONING OF A NOVEL 7TM RECEPTOR AXOR-2
FILE REFERENCE: GP-70433-C1
CURRENT APPLICATION NUMBER: US/09/760,354A
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/083,034
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: US 09/277,398
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 373
TYPE: PRT
ORGANISM: HOMO SAPIENS

Query Match 54.7%; Score 35; DB 10; Length 373;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
1 CFQLKKNMKV 10
|||
340 CFLNKLKK 349

RESULT 13

US-09-851-588-4
Sequence 4, Application US/09851588
Patent No. US20020042067A1
GENERAL INFORMATION:
APPLICANT: Mack, David
APPLICANT: Gish, Kurt C.
APPLICANT: Wilson, Keith E.
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
FILE REFERENCE: A-68829-1/DJB/JJD/AMS
CURRENT APPLICATION NUMBER: US/09/851,588
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/642,252
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: US 09/656,002
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 347
TYPE: PRT
ORGANISM: Homo sapiens
US-09-851-588-4

Query Match 53.1%; Score 34; DB 10; Length 347;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 OLKKNMKVR 12
::|||
DB 12 RVKKNLKKR 21

RESULT 14

US-10-046-935-2235
Sequence 2235, Application US/10046935
Patent No. US20020156011A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2235
LENGTH: 371
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: 197, 201, 203, 204
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-046-935-2235

Query Match 53.1%; Score 34; DB 9; Length 371;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 OLKKNMKVR 12
::|||
DB 12 RVKKNLKKR 21

RESULT 15

```

US-09-878-178-2235
; Sequence 2235, Application US/09878178
; Patent No. US2002017752A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; NUMBER OF SEQ ID NOS: 2237
; CURRENT FILING DATE: 2001-06-08
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2235
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(371)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-878-178-2235

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Query Match      53.1%; Score 34; DB 9; Length 371;
Best Local Similarity 60.0%; Pred. No. 1.ee+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 3 QLKQNMKKVR 12
Db 12 RVKQNLKKFR 21

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Search completed: February 21, 2003, 08:11:58
Job time : 6.88372 secs

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GenCore version 5.1.3
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M protein - protein search, using sw model
un on: February 21, 2003, 07:48:01 ; Search time 10.6047 Seconds
(without alignments)
108.784 Million cell updates/sec

file: US-09-743-107B-96
effect score: 64
sequence: 1 CFQLKKNMKYR 12

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

sarched: 283224 seqs, 96134422 residues
otal number of hits satisfying chosen parameters: 283224

inimum DB seq length: 0
aximum DB seq length: 2000000000
ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : PIR 73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	ID	Description
1	48	75.0	711	1 TFHUL	lactotransferrin p
2	42	65.6	351	2 S20078	NOV protein - chic
3	42	65.6	795	2 T34468	hypothetical prote
4	40	62.5	223	2 T37974	probable peroxisom
5	40	62.5	238	2 T40568	hypothetical prote
6	40	62.5	333	2 T29242	hypothetical prote
7	39	60.9	222	2 T48456	rna binding protei
8	39	60.9	282	2 A97214	uncharacterized co
9	39	60.9	339	2 D90106	hypothetical prote
10	39	60.9	409	2 S47440	secy protein - red
11	39	60.9	1162	2 T21557	hypothetical prote
12	39	60.9	1553	2 T18502	hypothetical prote
13	38	59.4	1166	2 A39432	ATP-dependent deox
14	38	59.4	2014	2 T21560	hypothetical prote
15	38	59.4	2021	2 A84771	similar to ch-TOG
16	37	57.8	22	2 S59071	secretory protein
17	37	57.8	224	2 C31201	GLI-related finger
18	37	57.8	267	2 S77802	hypothetical prote
19	37	57.8	335	2 T33211	hypothetical prote
20	37	57.8	510	2 G70162	conserved hypothet
21	37	57.8	546	2 A99600	conserved hypothet
22	37	57.8	718	2 T29708	hypothetical prote
23	37	57.8	784	1 IJHUC5	cadherin 5 precurs
24	36	56.2	81	2 E85172	hypothetical prote
25	36	56.2	81	2 E88038	hypothetical prote
26	36	56.2	104	2 D95003	hypothetical prote
27	36	56.2	191	2 B81220	cell filamentation
28	36	56.2	227	2 A59097	hypothetical prote
29	36	56.2	258	2 T00447	hypothetical prote

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61189; A31000; S741

R/Cho, Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: Preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R/Key, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; MUID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-448, 'T', 150-422, 'C', 424-711 <REY>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A/Reference number: A45401; MUID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIFP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; MUID:90326549; PMID:2374734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A/Reference number: S15853; MUID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <STI>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28, 'X', 30-31 <ST2>

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Query Match          65.6%; Score 42; DB 2; Length 351;
Best Local Similarity 66.7%; Pred. No. 9.5;
Matches      8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1  CFQLKKNMKKVR 12
DB      258  CIQTKSKMKAVR 269
          | | | | | | | |
          | | | | | | | |

RESULT 3
T34468
hypothetical protein ZK770.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34468
R:Maggi, L.; Gattung, S.; Bartko, L.
submitted to the EMBL Data Library, April 1997
A:Description: The sequence of C. elegans cosmid ZK770.
A:Reference number: Z21530
A:Accession: T34468
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-795 <MAG>
A:Cross-references: EMBL:U97404; PIDN:AA933303.1; GSPDB:GNO0019; CESP:ZK770.1
A:Experimental source: strain Bristol N2; clone ZK770
C:Genetics:
A:Gene: CESP:ZK770.1
A:Map position: 1
A:Introns: 18/1, 84/2, 125/3, 198/3; 257/3; 337/3; 378/3; 424/3; 477/2; 510/1; 563/

Query Match          65.6%; Score 42; DB 2; Length 795;
Best Local Similarity 70.0%; Pred. No. 20;
Matches      7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  CFQLKKNMKK 10
DB      329  CFQIKGNVKK 338
          | | | | | |
          | | | | | |

RESULT 4
T37974
probable peroxisomal membrane protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C:Accession: T37974
R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z21759
A:Accession: T37974
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-223 <MUR>
A:Cross-references: EMBL:Z69909; PIDN:CAA93785.1; GSPDB:GNO0066; SPDB:SPAC19G10.03c
A:Experimental source: strain 972h-; cosmid cl9G10
C:Genetics:
A:Gene: SPDB:SPAC19G10.03c
A:Map position: 1
A:Introns: 10/3; 170/2
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
C:Keywords: Peroxisome

Query Match          62.5%; Score 40; DB 2; Length 223;
Best Local Similarity 41.7%; Pred. No. 14;
Matches      5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY      1  CFQLKKNMKKVR 12
DB      140  CYELOQNSKKIK 151
          | : : : | | : :
          | : : : | | : :

RESULT 5
T40568

```

A;Cross-references: EMBL:AL162875
A;Experimental source: cultivar Columbia; BAC clone T32M21
C;Genetics:
A;Map position: 5
A;Introns: 38/3; 78/1; 96/3; 112/3; 145/2; 168/3; 205/3
A;Note: T32M21.200

Query Match 60.9%; Score 39; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LKKNMKKV 11
| | | | |
Db 9 LKKNMKKV 16

RESULT 8
A97214
uncharacterized conserved protein CAC2549 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C;Accession: A97214
R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A;Reference number: A96900; PMID:21359325; PMID:21359325
A;Accession: A97214
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-282 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK80500.1; PID:g15025572; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2549
C;Superfamily: Deinococcus radiodurans hypothetical protein DRB0099

Query Match 60.9%; Score 39; DB 2; Length 282;
Best Local Similarity 58.3%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOLKKNMKVR 12
| | | | | | | |
Db 241 CQOLKENTSKLR 252

RESULT 9
D90106
hypothetical protein orf339 [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: D90106
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reiter, R.
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; PMID:11323671; PMID:11323671
A;Accession: D90106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <DOU>
A;Cross-references: GB:AJ010592; NID:g12580683; PIDN:CAC27001.1; GSPDB:GN00151
C;Genetics:
A;Gene: orf339
A;Map position: 2
A;Genome: nucleomorph
C;Keywords: nucleomorph

Query Match 60.9%; Score 39; DB 2; Length 339;
Best Local Similarity 80.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FOLKKNMKKV 11

Db 179 FNLKKNKKV 188
|||||

RESULT 10

S47440
secY protein - red alga (Cyanidium caldarium)
C:Species: Cyanidium caldarium
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
C:Accession: S47440
R:Vogel, H.; Valentin, K.
submitted to the EMBL Data Library, August 1994
A:Reference number: S47440
A:Accession: S47440
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <VOG>
A:Cross-references: EMBL:Z36235; NID:G529651; PIDN:CAA85270.1; PID:G529652
C:Superfamily: preprotein translocase secY

Query Match

Best Local Similarity 60.9%; Score 39; DB 2; Length 409;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOLKKNKK 10
|||

Db 312 CFELSNLKK 321
|||

RESULT 11

T21557
hypothetical protein F29G6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T21557
R:Haris, B.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19441
A:Accession: T21557
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1162 <WIL>
A:Cross-references: EMBL:Z78543; PIDN:CAB01753.1; GSPDB:GN000028; CBSP:F29G6.1
A:Experimental source: clone F29G6
C:Genetics:
A:Gene: CBSP:F29G6.1
A:Map position: X
A:Introns: 51/1; 78/1; 132/2; 161/1; 236/3; 276/3; 318/3; 359/3; 397/3; 470/3; 54

Query Match

Best Local Similarity 60.9%; Score 39; DB 2; Length 1162;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOLKKNKKV 12
|||

Db 943 CIQKKNKTIQ 954
|||

RESULT 12

T18502
hypothetical protein C0755c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T18502
R:Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z18935
A:Accession: T18502
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1553 <LAW>
A:Cross-references: EMBL:Z98551; NID:G1331903; PID:G1331923; PIDN:CAB11141.1
C:Genetics:

Query Match

Best Local Similarity 63.6%; Score 38; DB 2; Length 1166;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FOLKKNKKV 12
|||

Db 486 FOLQKMKKAK 496
|||

A:Map position: 3
A>Note: C0755c

Query Match 50.9%; Score 39; DB 2; Length 1553;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LKKNKKV 12
|||||

Db 39 MKKNKKV 47
|||||

RESULT 13

A39432
ATP-dependent deoxyribonuclease chain B - Bacillus subtilis
N:Alternate names: ATP-dependent exonuclease synthesis protein AddB
C:Species: Bacillus subtilis
C>Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 02-Feb-2001
C:Accession: A39432; S61272; A69583
R:Kooistra, J.; Venema, G.
J. Bacteriol. 173, 3644-3655, 1991
A:Title: Cloning, sequencing, and expression of Bacillus subtilis genes involved in ATP-
A:Reference number: A39432; MUID:91267926; PMID:1646786
A:Accession: A39432
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1166 <KOO>
A:Cross-references: GB:M63489; NID:G142438; PIDN:AAA22200.1; PID:G142439
R:Haigema, B.J.; Hamoen, L.W.; Kooistra, J.; Venema, G.; van Sinderen, D.
Mol. Microbiol. 15, 203-211, 1995
A:Title: Expression of the ATP-dependent deoxyribonuclease of Bacillus subtilis is under
A:Reference number: S61272; MUID:95264907; PMID:7746142
A:Accession: S61272
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-13 <HAI>
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maguda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69583
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1166 <KUN>
A:Cross-references: GB:Z99109; GB:AL009126; NID:G2633260; PIDN:CAB12902.1; PID:G2633398
A:Experimental source: strain 168
C:Genetics:
A:Gene: addB
C:Superfamily: Bacillus subtilis ATP-dependent deoxyribonuclease chain B
C:Keywords: nucleotide binding; P-loop
F:8-15/Region: nucleotide-binding motif A (P-loop)

LT 14
360
theoretical protein T25C12.3 - Caenorhabditis elegans
ecies: Caenorhabditis elegans
te: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
cession: T21560; T23053; T25270
arris, B.
itted to the EMBL Data Library, August 1996
ference number: Z19441
cession: T21560
atus: preliminary; translated from GB/EMBL/DDBJ
ecule type: DNA
sidues: 1-2014 <WIL>
oss-references: EMBL:Z78543; PIDN:CAB01757.1; GSPDB:GN000028; CESP:T25C12.3
erimental source: clone F29G6
ite, S.
itted to the EMBL Data Library, April 1997
ference number: Z19664
cession: T23053
atus: preliminary; translated from GB/EMBL/DDBJ
ecule type: DNA
sidues: 1-2014 <W12>
oss-references: EMBL:Z93779; PIDN:CAB07849.1; GSPDB:GN000028; CESP:T25C12.3
erimental source: clone H06X08
rshaw, J.
itted to the EMBL Data Library, November 1995
ference number: Z20007
cession: T25270
atus: preliminary; translated from GB/EMBL/DDBJ
ecule type: DNA
sidues: 1-2014 <W13>
oss-references: EMBL:Z66566; PIDN:CAA91487.1; GSPDB:GN000028; CESP:T25C12.3
erimental source: clone T25C12
netics:
ne: CESP:T25C12.3
p position: X
trons: 10/2; 91/3; 136/1; 159/2; 182/3; 203/1; 225/3; 280/1; 422/3; 466/3; 559/3; 69
722/1; 1779/3; 1843/3; 1908/2; 1941/2; 2007/2
ery Match 59.4%; Score 38; DB 2; Length 2014;
st Local Similarity 87.5%; Pred. No. 2.3e+02;
atches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
2 FOLKKNMK 9
|||||:
1410 FOLKKNLK 1417
LT 15
71
lar to ch-TOG protein from Homo sapiens [imported] - Arabidopsis thaliana
ecies: Arabidopsis thaliana (mouse-ear cress)
te: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
cession: A84771
n, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
re 402, 761-768, 1999
tle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
ference number: A84420; MUID:20083487; PMID:10617197
cession: A84771
atus: preliminary
ecule type: DNA
sidues: 1-2021 <STO>
oss-references: GB:AE002093; NID:G4263790; PIDN:AD15450.1; GSPDB:GN00139
netics:
ne: At2g35630
p position: 2
ery Match 59.4%; Score 38; DB 2; Length 2021;
st Local Similarity 58.3%; Pred. No. 2.3e+02;
atches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 CFOLKKNMKVR 12
|:|:|:
Db 1405 CFRLAKDMKRR 1416
Search completed: February 21, 2003, 08:02:51
Job time : 12.6047 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

M protein - protein search, using sw model

un on: February 21, 2003, 07:28:06 ; Search time 5.2093 Seconds
(without alignments)
95.544 Million cell updates/sec

itle: US-09-743-107B-96

effect score: 64

sequence: 1 CFQLKKNMKVYR 12

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 112892 seqs, 41476328 residues

total number of hits satisfying chosen parameters: 112892

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	ID	Description
1	48	75.0	711	1 TRFL_HUMAN	P02788 homo sapien
2	42	65.6	351	1 NOV_CHICK	P26686 gallus gall
3	42	65.6	573	1 UR1_LACPE	P26929 lactobacilli
4	42	65.6	795	1 DE97_CAEEL	O01635 caenorhabdi
5	41	64.1	695	1 TRFL_HORSE	O77811 equus cabal
6	40	62.5	238	1 YBN9_SCHPO	Q10333 schizosacch
7	39	60.9	410	1 SECY_CVACA	P46249 cyanidium c
8	38	59.4	353	1 NOV_COTJA	P32642 coturnix co
9	38	59.4	1166	1 ADDE_BACSU	P23477 bacillus su
10	37	57.8	267	1 Y125_MYCCA	P33661 mycoplasma
11	37	57.8	510	1 Y504_BORBU	O51457 borrelia bu
12	37	57.8	697	1 HKR1_HUMAN	P10072 homo sapien
13	37	57.8	708	1 TRFL_CAMDR	Q8tun0 camelus dro
14	37	57.8	784	1 CAD5_HUMAN	P31151 homo sapien
15	36	56.2	282	1 YEAS_YEAST	P40003 saccharomyc
16	36	56.2	258	1 TRMU_CHLFR	O84289 chlamydia t
17	36	56.2	560	1 VNUC_INBLR	P04665 influenza b
18	36	56.2	566	1 SYR_METJA	Q57689 methanococc
19	35	54.7	175	1 BGLJ_ECOLI	P39404 escherichia
20	35	54.7	195	1 NUC_EORBU	O51372 borrelia bu
21	35	54.7	352	1 RECF_TREPA	O83049 treponema p
22	35	54.7	373	1 SRB3_HUMAN	Q9n866 homo sapien
23	35	54.7	373	1 SRB3_RAT	Q9j112 rattus norv
24	35	54.7	414	1 Y701_METJA	Q88112 methanococc
25	35	54.7	656	1 YC26_PORFU	P31392 porphyra pu
26	35	54.7	1008	1 SN14_YEAST	P36048 saccharomyc
27	35	54.7	4967	1 RYR2_HUMAN	Q92736 homo sapien
28	34	53.1	126	1 RK12_CVAPA	P48124 cyanophora
29	34	53.1	174	1 FTRV_SPIOL	P38365 spinacia ol
30	34	53.1	181	1 TRIF_HUMAN	P48788 homo sapien
31	34	53.1	181	1 TRIF_MOUSE	P13412 mus musculu
32	34	53.1	181	1 TRIF_RABIT	P02643 oryctolagus
33	34	53.1	181	1 TRIF_RAT	P27768 rattus norv

ALIGNMENTS

RESULT 1	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
ID	AC	Q96KZ5;	Q16780; Q16785; Q16786; Q16789; Q00756; Q9H1Z3; Q96KZ4;	
DT	21-JUL-1986	(Rel. 01, Created)		
DT	15-JUL-1999	(Rel. 38, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferrroxin A;			
DE	Lactoferrroxin B; Lactoferrroxin C].			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]	SEQUENCE FROM N.A.		
RP	TISSUE=Mammary gland;			
RC	MEDLINE=90384839; PubMed=2402455;			
RX	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;			
RA	"Complete nucleotide sequence of human mammary gland lactoferrin.";			
RT	Nucleic Acids Res. 18:5288-5288(1990).			
RL	[2]	SEQUENCE FROM N.A.		
RP	TISSUE=Mammary gland;			
RC	Choi Y.Y.;			
RA	Thesis (1994), Genetic Engineering Research Institute / Taejeon, Korea.			
RN	[3]	SEQUENCE FROM N.A.		
RP	Conceely O.M.;			
RA	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RL	[4]	SEQUENCE FROM N.A.		
RP	TISSUE=Mammary gland;			
RC	Liang Q., Jimenez-Flores R., Richardson T.;			
RA	"Molecular cloning and sequence analysis of human lactoferrin.";			
RT	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]	SEQUENCE FROM N.A.		
RP	TISSUE=Bone marrow;			
RC	Wei X., Han J., Rado T.A.;			
RA	"Human neutrophil lactoferrin coding and 5' flanking region DNA			
RT	sequences.";			
RN	[6]	SEQUENCE FROM N.A.		
RP	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RL	[7]	SEQUENCE FROM N.A.		
RP	TISSUE=Mammary gland;			
RC	Cheng H., Chen X., Huan L.;			
RA	"cDNA cloning and sequence analysis of human lactoferrin.";			
RT	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[8]	SEQUENCE FROM N.A.		
RP	TISSUE=Prostate;			
RC	Strausberg R.;			
RA	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RL	[8]			

34 34 53.1 228 1 YDFH_ECOLI P77577 escherichia
35 34 53.1 252 1 YC88_METJA Q58684 methanococc
36 34 53.1 297 1 YG1B_YEAST P53210 saccharomyc
37 34 53.1 387 1 SRB3_BRARE Q91918 brachydanio
38 34 53.1 560 1 VNUC_INBAA P11102 influenza b
39 34 53.1 560 1 VNUC_INBAC P13884 influenza b
40 34 53.1 560 1 VNUC_INBAD P13885 influenza b
41 34 53.1 560 1 VNUC_INBP9 Q36433 influenza b
42 34 53.1 560 1 VNUC_INBSI P04666 influenza b
43 34 53.1 585 1 D170_HUMAN Q16204 homo sapien
44 34 53.1 659 1 HEPA_HSV7J P52376 human herpe
45 34 53.1 1562 1 RPOD_CHLVU P12465 chlorella v

RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE-Mammary gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RL "Nucleotide sequence of human lactoferrin cDNA.";
RN Nucleic Acids Res. 18:4013-4013(1990).
RP SEQUENCE OF 20-711.
RX MEDLINE=8507667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RG Legrand D., Spik G., Montreuil J., Jolles P.;
RL "Human lactoferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RN Eur. J. Biochem. 145:659-666(1984).
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RG Jolles P.;
RL "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RN N- and C-terminal domains.";
RX Biochim. Biophys. Acta 670:243-254(1981).
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RG Jolles P.;
RL "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin.";
RN FEBS Lett. 142:107-110(1982).
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=8800103; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RL "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RN Blood 70:989-993(1987).
RP SEQUENCE OF 237-711 FROM N.A.
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RN Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Baside M., Kaplan N., Greco T., Touchman J., Muzny D.,
RG Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RG Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sacripanti J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE OF 237-711 FROM N.A.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RL "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RN J. Mol. Biol. 209:711-734(1989).
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RG Baker E.N.;
RL "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RN 253--methionine mutant.";
RX Biochemistry 36:1341-1346(1997).
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RL "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RX Acta Crystallogr. D 55:403-407(1999).
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RL "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change.";
RN Acta Crystallogr. D 54:1319-1335(1998).
RP CHARACTERIZATION OF LACTOFERRINS.
RX MEDLINE=9116929; PubMed=1369293;
RA Tani F., Iio K., Chiba H., Yoshikawa M.;
RL "Isolation and characterization of opioid antagonist peptides derived
RT from human lactoferrin.";
RN Agric. Biol. Chem. 54:1803-1810(1990).
RP VARIANTS THR-30 AND ARG-48.
RX PubMed=9873069;
RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RG Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
RG El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hejtmancik J.F., Teng C.F.;
RL "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RN Mol. Vision 4:31-32(1998).
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- FUNCTION: LACTOFERRIN A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERRIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERRIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X53961; CAA37914.1; -
CC EMBL; U07643; AAB60324.1; -
CC EMBL; M93150; AAA36159.1; -
CC EMBL; M83202; AAA59511.1; -
CC EMBL; M83205; AAA58656.1; -
CC EMBL; M18642; AAA86665.1; -
CC EMBL; AF332168; AAG48753.1; -
CC EMBL; BC015822; AAH15822.1; -
CC EMBL; BC015823; AAH15823.1; -
CC EMBL; M73700; AAA59479.1; -
CC EMBL; X52941; CAA37116.1; -
CC EMBL; U95626; AAB57795.1; -
CC PIR; S11228; TPNUD.
CC PDB; 1LCF; 31-AUG-94.
CC PDB; 1LCT; 31-OCT-93.
CC PDB; 1LFG; 31-JUL-94.
CC PDB; 1LFG; 31-OCT-93.
CC PDB; 1LFI; 31-OCT-93.
CC PDB; 1LGB; 31-AUG-94.
CC PDB; 1LGC; 31-AUG-94.
CC PDB; 1BKA; 08-NOV-96.
CC PDB; 1DSN; 08-MAR-96.
CC PDB; 1HSE; 12-MAR-97.
CC PDB; 1VFD; 21-APR-97.

Query Match 75.0%; Score 48; DB 1; Length 711;
 Best Local Similarity 66.7%; Pred. No. 0.62;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 CFOLKKNMKVR 12
 |||:::|||||
 39 CFQWQNMKVR 50

350 CHICK STANDARD; PRT; 351 AA.
 228566; Score 42; DB 1; Length 351;
 01-DEC-1992 (Rel. 24, Created)
 01-DEC-1992 (Rel. 24, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 NOV protein precursor (Nephroblastoma overexpressed gene protein).
 NOV.
 Gallus gallus (Chicken).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Gallus.
 NCBI_TaxID=9031;
 [1]
 SEQUENCE FROM N.A.
 STRAIN-Brown leghorn;
 MEDLINE=92107157; PubMed=1309586;
 Joliot V., Martinerie C., Dambrine G., Plassiat G., Brisac M.,
 Crochet J., Perbal B.;
 "Provitamin rearrangements and overexpression of a new cellular gene
 (nov) in myeloblastosis-associated virus type 1-induced
 nephroblastomas";
 Mol. Cell. Biol. 12:10-21(1992).

-!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
 GROWTH REGULATION. ITS OVEREXPRESSION IS ASSOCIATED WITH
 TUMORIGENESIS AND EXPRESSION OF A N-TERMINAL-TRUNCATED VERSION
 OF NOV GENE IN CHICKEN EMBRYONIC FIBROBLASTS (CEP) IS SUFFICIENT
 TO INDUCE THE TRANSFORMATION OF CEP IN VITRO.
 -!- TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN
 MUSCLE AND INTESTINE, IN THE EMBRYO. LONG AND LESS SO IN BRAIN AND
 SPLEEN, IN ADULT CHICKEN.
 -!- DEVELOPMENTAL STAGE: MAVI-INDUCED NEPHROBLASTOMAS EXPRESS A HIGH
 LEVEL OF NOV GENE WHOSE TRANSCRIPTION IS NORMALLY ARRESTED IN
 ADULT KIDNEY.
 -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 PROTEIN FAMILY. CEP-10/CYR61/CTGF/FISP-12/NOV PROTEIN SUBFAMILY.
 -!- SIMILARITY: CONTAINS 1 WFEC DOMAIN.
 -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.

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 EMBL; X59284; CAA41975.1; --
 PIR; S20078; S20078.
 InterPro; IPR000359; Cys knot.
 InterPro; IPR000867; Ins1_gro_fac_pr.
 InterPro; IPR000884; TSF1.
 InterPro; IPR001007; VWF C.
 Pfam; PF00007; Cys knot; 1.
 Pfam; PF00090; tsf_1; 1.
 Pfam; PF00093; vwf_1; 1.
 Pfam; PF00219; IGFBP; 1.
 SMART; SM00041; CT; 1.
 SMART; SM00121; IB; 1.
 SMART; SM00209; TSF1; 1.
 SMART; SM00214; VWC; 1.
 PROSITE; PS00222; IGF_BINDING; 1.

DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS01208; VWF_C; 1.
 KW Proto-oncogene; Growth factor binding; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 351 NOV PROTEIN.
 FT DOMAIN 104 170 WFEC.
 FT DOMAIN 258 332 CTCK.
 FT DISULFID 258 295 BY SIMILARITY.
 FT DISULFID 275 309 BY SIMILARITY.
 FT DISULFID 286 325 BY SIMILARITY.
 FT DISULFID 289 327 BY SIMILARITY.
 FT DISULFID 294 331 BY SIMILARITY.
 FT CARBOHYD 274 274 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 351 AA; 38268 MW; 1ECB3FA3058C6797 CRC64;

Query Match 65.6%; Score 42; DB 1; Length 351;
 Best Local Similarity 66.7%; Pred. No. 3.5;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOLKKNMKVR 12
 |||:::|||||
 DB 258 CIQTKSKMKVR 269

RESULT 3
 UREL_LACFE STANDARD; PRT; 573 AA.
 ID UREL_LACFE
 AC P26929;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acid urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase).
 GN UREC.
 OS Lactobacillus fermentum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 NCBI_TaxID=1613;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=JCM 5869;
 RA Suzuki K., Takahashi M., Imamura S., Ishikawa T.;
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
 CC -!- PM: Lys-222 is carbamylated. The carbamoyl group provides the
 ligands for the two nickel ions (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE UREASE FAMILY.

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 EMBL; D10605; BAA01460.1; --
 HSSP; P41020; UEBP.
 MEROPS; M38.UNW; --
 InterPro; IPR001924; UreaseA.
 Pfam; PF00449; urease; 1.
 Pfam; PF02802; urease_C; 1.
 ProDom; PD002467; UreaseA; 1.
 DR PROSITE; PS00145; UREASE_2; 1.
 DR PROSITE; PS01120; UREASE_1; 1.
 KW Hydrolase; Metal-binding; Nickel.
 FT METAL 139 139 NICKEL 2 (BY SIMILARITY).
 FT METAL 141 141 NICKEL 2 (BY SIMILARITY).
 FT METAL 222 222 NICKEL 1 AND 2 (BY SIMILARITY).
 FT METAL 251 251 NICKEL 1 (BY SIMILARITY).
 FT METAL 277 277 NICKEL 1 (BY SIMILARITY).

PT METAL 365 365 NICKEL 2 (BY SIMILARITY).
 PT ACT SITE 325 325 BY SIMILARITY.
 IQ SEQUENCE 573 AA; 61805 MW; 2D2619781C39E54B CRC64;

Query Match 55.6%; Score 42; DB 1; Length 573;
 Best Local Similarity 56.7%; Pred. No. 5.5;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Y 1 CFQLKKNMKYR 12
 :|||
 b 379 CQQLASKMKYR 390

RESULT 4
 DEGY CAEEL STANDARD; PRT; 795 AA.
 IC 001635;
 VT 15-JUL-1998 (Rel. 36, Created)
 VT 15-JUN-1998 (Rel. 36, Last sequence update)
 JT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Degenerin-like protein ZK770.1 in chromosome I.
 N ZK770.1.
 S Caenorhabditis elegans.
 C Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
 C Rhabditidae; Pelodierinae; Caenorhabditis.
 X NCBI_TaxID=6239;
 N [1]
 P SEQUENCE FROM N.A.
 C STRAIN=Bristol N2;
 A Maggi L., Gattung S., Bartko L.;
 L Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 C -1- SUBCELLULAR LOCATION: Integral membrane protein.
 C -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL FAMILY.

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EMBL; U97404; AAB93309.1; --
 WormPep; ZK770.1; CE15411.
 R InterPro; IPR004726; Deg-1.
 R InterPro; IPR001873; Na-channel_ASC.
 R Pfam; PF00858; ASC; 1.
 R PRINTS; PRO1078; AMINACHANNEL.
 R TIGRFAMs; TIGR00867; deg-1; 1.
 R PROSITE; PS01206; ASC; 1.
 M Hypothetical protein; Ionic channel; Transmembrane; Ion transport; Glycoprotein.
 M DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).
 T TRANSMEM 59 79 POTENTIAL.
 T DOMAIN 80 739 EXTRACELLULAR (POTENTIAL).
 T TRANSMEM 740 760 POTENTIAL.
 T DOMAIN 761 795 CYTOPLASMIC (POTENTIAL).
 T CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 T CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
 T CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 T CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 T CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
 T CARBOHYD 518 518 N-LINKED (GLCNAC. . .) (POTENTIAL).
 Q SEQUENCE 795 AA; 90776 MW; 2CAACF7D41770B54 CRC64;

Query Match 55.6%; Score 42; DB 1; Length 795;
 Best Local Similarity 70.0%; Pred. No. 7.4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQLKKNMKK 10
 :|||
 b 329 CFQIKGNVKK 338

RESULT 5
 TRFL HORSE STANDARD; PRT; 695 AA.
 AC 077811;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DB Lactotransferrin precursor (Lactoferrin) (Fragment).
 GN LTF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CX NCBI_TaxID=9796;
 RN [1]
 P SEQUENCE FROM N.A.
 R Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RA "CDNA sequence of mare lactoferrin";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Milk;
 RX MEDLINE=99296631; PubMed=10366507;
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "Three-dimensional structure of mare diferric lactoferrin at 2.6-A resolution.";
 RT J. Mol. Biol. 289:303-317(1999).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 EMBL; AJ010930; CAA09407.1; --
 DR PDB; 1BIX; 02-DEC-98.
 DR PDB; 1B7U; 02-FEB-99.
 DR PDB; 1B7Z; 02-FEB-99.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PRO0422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 1.
 M Signal; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.
 M NON_TER 1 6
 M SIGNAL <1 6 LACTOTRANSFERRIN.
 M CHAIN 7 695
 M REPEAT 7 350 1.
 M REPEAT 351 695 2.
 M FT DISULFID 15 51
 M FT DISULFID 25 42
 M FT DISULFID 121 204
 M FT DISULFID 163 179
 M FT DISULFID 186 189
 M FT DISULFID 176 187
 M FT DISULFID 237 251
 M FT DISULFID 354 386
 M FT DISULFID 364 377
 M FT DISULFID 411 690
 M FT DISULFID 431 653

Nature 415:871-880(2002).

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EMBL; AL096788; CAB46672.1; -
Hypothetical protein.

Query Match 62.5%; Score 40; DB 1; Length 238;
Best Local Similarity 41.7%; Pred. No. 5.5;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFOLKKMKVKVR 12
|::||::|
Db 155 CYELOQNSKKIK 166

RESULT 7
SECY_CVACA STANDARD; PRT; 410 AA.
ID SECY_CVACA STANDARD; PRT; 410 AA.
AC P46249; Q9MD55;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Preprotein translocase secy subunit.
GN SECY.
OS Cyanidium caldarium.
OC Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
OX NCBI_TaxID=2771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RK-1.
RX MEDLINE=97134960; PubMed=8980520;
RA Vogel H., Fischer S., Valentini K.-U.;
RT "A model for the evolution of the plastid sec apparatus inferred from
secy gene phylogeny."
RL Plant Mol. Biol. 32:685-692(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RK-1;
RX MEDLINE=20496959; PubMed=11040290;
RA Gloeckner G., Rosenthal A., Valentini K.-U.;
RT "The structure and gene repertoire of an ancient red algal plastid
genome."
RL J. Mol. Evol. 51:382-390(2000).
CC -!- FUNCTION: INVOLVED IN PROTEIN EXPORT. PROBABLY INTERACTS WITH
OTHER PROTEINS TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE
CHLOROPLAST ENDOPLASMIC RETICULUM (CER) MEMBRANES.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast.
CC -!- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
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EMBL; AF022186; AAF12924.1; -
InterPro; IPR002208; SecY.
Fam; PF00344; SecY; 1.
DR PRINTS; PR00303; SECYTNNLCASE.
DR TIGRFAMs; TIGR00967; 3a0501s007; 1.
DR PROSITE; PS00755; SECY 1; 1.

T DISULFID 463
T DISULFID 487
T DISULFID 497
T DISULFID 508
T DISULFID 579
T DISULFID 631
T METAL 66
T METAL 98
T METAL 198
T METAL 259
T METAL 401
T METAL 439
T METAL 532
T METAL 601
T BINDING 127
T BINDING 127
T CARBOHYD 143
T CARBOHYD 287
T CARBOHYD 482
Q SEQUENCE 695 AA; 75991 MW; 07BB84D50E1B165D CRC64;

Query Match 54.1%; Score 41; DB 1; Length 695;
Best Local Similarity 58.3%; Pred. No. 9.8;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Y 1 CFOLKKMKVKVR 12
|::||::|
Z 25 CAKFQNMKVKVR 36

RESULT 6
YEM9_SCHPO STANDARD; PRT; 238 AA.
ID YEM9_SCHPO STANDARD; PRT; 238 AA.
AC Q10333;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C582.09 in chromosome II.
GN SPBC582.09.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
SGours K., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett B., Odell C.,
Olivier K., O'Neill S., Pearson D., Quail M.A., Rabbinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skellton J., Simmonds M., Squares R., Squares K., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
Borzum K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedler H., Mambutt R., Purnelle B.,
Goiffau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Domínguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
The genome sequence of Schizosaccharomyces pombe."

DR PROSITE, PS00756; SECY 2; 1.
 KW Protein transport; Transmembrane; Chloroplast; Translocation.
 FT CONFLICT 149 MISSING (IN REF. 1).
 SQ SEQUENCE 410 AA; 46242 MW; 7CB0130175BIDF03 CRC64;

Query Match 60.9%; Score 39; DB 1; Length 410;
 Best Local Similarity 60.0%; Pred. No. 13;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFQLEKNNKK 10
 ||:|:|:|:
 Db 313 CFELSNLKK 322

RESULT 8
 ID NOV_COTJA STANDARD; PRT; 353 AA.
 AC P42642;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE NOV protein precursor (Nephroblastoma overexpressed gene protein).
 GN NOV.
 OS Coturnix coturnix japonica (Japanese quail).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 CC Coturnix.
 DX NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Weiskirchen R., Bister K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
 CC GROWTH REGULATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC PROTEIN FAMILY. CEP-10/CYR61/CTGF/FISP-12/NOV PROTEIN SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 VWFc DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.
 CC -----
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 CC -----

EMBL; U13063; AAA2128.1; -
 InterPro; IPR000359; Cys_knot.
 InterPro; IPR000867; Insl_gro_fac_pr.
 InterPro; IPR000884; TSPI.
 InterPro; IPR001007; VWF_C.
 Pfam; PF00007; Cys_knot_1.
 Pfam; PF00090; tspl_1.
 Pfam; PF00093; wvc_1.
 Pfam; PF00219; IGFBP_1.
 SMART; SM00041; CT; 1.
 SMART; SM00121; IB; 1.
 SMART; SM00209; TSPI; 1.
 SMART; SM00214; VWC; 1.
 PROSITE; PS00222; IGF BINDING; 1.
 PROSITE; PS01185; CTCK_1; 1.
 PROSITE; PS01225; CTCK_2; 1.
 PROSITE; PS01208; VWFc; 1.
 PROSITE; PS01208; VWFc; 1.
 T T Proto-oncogene; Growth factor binding; signal.
 T T SIGNAL 1 26
 T T CHAIN 27 353
 T T DOMAIN 106 172
 T T DOMAIN 260 334
 T T CTCK.
 T T BY SIMILARITY.
 T T DISULFID 260 297
 T T BY SIMILARITY.
 T T DISULFID 277 311
 T T BY SIMILARITY.
 T T DISULFID 288 327
 T T BY SIMILARITY.
 T T DISULFID 291 329

FT DISULFID 296 333 BY SIMILARITY.
 FT CARBOHYD 276 276 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 353 AA; 38667 MW; 7179F8533882E89 CRC64;

Query Match 59.4%; Score 38; DB 1; Length 353;
 Best Local Similarity 58.3%; Pred. No. 17;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQLEKNNKKYR 12
 ||:|:|:|:
 Db 260 CIRTKGKMKAVR 271

RESULT 9
 ID ADDB_BACSU STANDARD; PRT; 1166 AA.
 AC P23477;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ATP-dependent nuclease subunit B.
 GN ADDB.
 OS Bacillus subtilis.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kocistira J., Venema G.;
 RL MEDLINE=91267926; PubMed=1646786;
 RC STRAIN=OG1;
 RT "Cloning, sequencing, and expression of Bacillus subtilis genes
 RT involved in ATP-dependent nuclease synthesis.";
 RL J. Bacteriol. 173:3644-3655(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.;
 RC STRAIN=168;
 RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RL MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borrias R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Guiseppe G., Guy B.J., Goffeau A., Golightly E.J., Grandi G.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mabel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Furnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche B., Roche M., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Serot S.J., Serter P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).

1- FUNCTION: THE ENZYME COMPLEX MAY HAVE A WIDE VARIETY OF CATALYTIC
 ACTIVITIES INCLUDING ATP-DEPENDENT EXONUCLEASE, ATP-STIMULATED
 ENDONUCLEASE, ATP-DEPENDENT HELICASE AND DNA-DEPENDENT ATPASE
 ACTIVITIES.
 2- SUBUNIT: THE B-SUBUNIT IS ATP-DEPENDENT NUCLEASE COMPLEX IS FORMED
 BY ONE B SUBUNIT IN CONJUNCTION WITH ONE A SUBUNIT.
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 or send an email to license@isb-sib.ch).
 4- EMBL: M63489; AAB22200.1; --
 EMBL: Y14081; CA474481.1; --
 EMBL: Z99109; CAB12902.1; --
 PIR: A39432; A39432.
 Subtilist; BG10465; addB.
 InterPro: IPR000212; UvrD-helicase.
 Pfam: PF00580; UvrD-helicase; 1.
 Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
 DNA repair; Complete proteome.
 NP BIND 1 22 ATP (POTENTIAL).
 Q SEQUENCE 1166 AA; 134631 MW; 1A57BBE81A08AB4A CRC64;
 Query Match 59.4%; Score 38; DB 1; Length 1166;
 Best Local Similarity 63.6%; Pred. No. 51;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Y 2 FOLKXNMKKVR 12
 |||:||||:
 b 486 FOLKXNMKKAK 496
 RESULT 10
 125 MYCCA STANDARD; PRT; 267 AA.
 D Y125 MYCCA
 C PS3661;
 T 01-OCT-1996 (Rel. 34, Created)
 T 01-OCT-1996 (Rel. 34, Last sequence update)
 T 01-OCT-1996 (Rel. 34, Last annotation update)
 E Hypothetical protein (Fragment).
 S Mycoplasma capricolum.
 C Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
 C Entomoplasmataceae.
 X NCBI_TaxID=2095;
 N [1]
 P SEQUENCE FROM N.A.
 C STRAIN=ATCC 27343 / KID;
 X MEDLINE=96059641; PubMed=7476192;
 A Bork P., Ouzounis C., Casari G., Schneider R., Sander C.,
 Dolan M., Gilbert W., Gillevet P.M.,
 "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
 its physiology".
 T Mol. Microbiol. 16:955-967(1995).
 L
 1- SIMILARITY: BELONGS TO THE COF/YBHA/YIDA/YIGL (E. COLI) / YCSE/YXEH
 (B. SUBTILIS) FAMILY.
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 3- EMBL: Z33006; CA483689.1; --
 InterPro: IPR001454; Hlgnaase/hydrolase.
 X InterPro: IPR000150; Hypothet. cof.
 X Pfam: PF00702; Hydrolase; 1.
 X PROSITE: PS01228; COF_1; 1.

DR PROSITE; PS01229; COF_2; 1.
 KW Hypothetical protein.
 FT NON TER 267
 SQ SEQUENCE 267 AA; 30425 MW; D5912DD5B39A8451 CRC64;
 Query Match 57.8%; Score 37; DB 1; Length 267;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CFOLKXNMKKVR 12
 |||:||||:
 Db 158 CFGKKNRQMR 169
 RESULT 11
 Y504 BORBU STANDARD; PRT; 510 AA.
 ID Y504 BORBU
 AC OS1457;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein BB0504.
 GN BB0504.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 CC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 CX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Hanson M.,
 Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman C.,
 Utterback T., Wathley L., McDonald L., Artiach P., Bowman C.,
 Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 Smith H.O., Venter J.C.;
 RA "Genomic sequence of a Lyme disease spirochete, Borrelia
 burgdorferi".
 RT Nature 390:580-586(1997).
 RL
 CC -!- SIMILARITY: BELONGS TO THE UPF0144 FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 HD DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 KH DOMAIN.
 CC
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 3- EMBL: AE001153; AAC66875.1; --
 TIGR: BB0504;
 DR InterPro: IPR002819; HD.
 DR InterPro: IPR004087; KH dom.
 DR InterPro: IPR004088; KH type 1.
 DR InterPro: IPR003607; ME Pplase_Hdc.
 DR Pfam: PF00013; KH-domain; 1.
 DR Pfam: PF01966; HD; 1.
 DR SMART; SM00471; Hdc; 1.
 DR SMART; SM00322; KH; 1.
 DR TIGRFAMs; TIGR00277; HDIG; 1.
 DR PROSITE; PS50084; KH TYPE 1; 1.
 KW Hypothetical protein; Transmembrane; RNA-binding; Complete proteome.
 FT TRANSMEM 2 22 POTENTIAL.
 FT DOMAIN 197 265 KH.
 FT DOMAIN 324 419 HD.
 SQ SEQUENCE 510 AA; 58002 MW; A95D675FEAG3C668 CRC64;
 Query Match 57.8%; Score 37; DB 1; Length 510;
 Best Local Similarity 77.8%; Pred. No. 36;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LKNNKKVR 12
 DB 31 LKNNKKVR 39

RESULT 12
 HKR1_HUMAN
 ID HKR1_HUMAN STANDARD; PRT; 697 AA.
 AC P10072; Q9UM09;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Krueppel-related zinc finger protein 1 (HKR1 protein) (Fragment).
 GN HKR1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Oguri T., Katoh O., Takahashi T., Isobe T., Kuramoto K., Hirata S.,
 RA Yamakido M., Watanabe H.;
 RT "The krueppel-type zinc finger family gene, HKR1, is induced in lung
 RT cancer by exposure to platinum drugs.";
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 314-537 FROM N.A.
 RX MEDLINE=8906896; PubMed=2850480;
 RA Rupert J.M., Kinzler K.W., Wong A.J., Bigner S.H., Kao F.T.,
 RA Law M.L., Seunav H.N., O'Brien S.J., Vogelstein B.;
 RT "The Gli-Kruppel family of human genes.";
 RL Mol. Cell. Biol. 8:3104-3113(1988).
 CC -!- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC -!- SIMILARITY: CONTAINS 1 KRAB DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; AB013897; BAA96058.1; -;
 CC EMBL; M20675; -; NOT_ANNOTATED_CDS.
 CC PIR; C31201; C31201.
 CC HSP; P08047; 18P2.
 CC Genew; HGNC:4928; HKR1.
 CC MIM; 165250;
 CC InterPro; IPR001909; KRAB.
 CC InterPro; IPR000822; Znf_C2H2.
 CC Pfam; PF00096; zf-C2H2; 13.
 CC Pfam; PF01352; KRAB; 1.
 CC SMART; SM00349; KRAB; 1.
 CC SMART; SM00355; Znf_C2H2; 13.
 CC PROSITE; PS00805; KRAB; 1.
 CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.
 CC PROSITE; PS0157; ZINC_FINGER_C2H2_2; 13.
 CC Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 CC Nuclear protein; Repeat.
 CC NON_TER 1
 CC DOMAIN 71 142 KRAB.
 CC DOMAIN 339 695 ZINC_FINGERS.
 CC ZN_FING 339 361 C2H2-TYPE.
 CC ZN_FING 367 389 C2H2-TYPE.
 CC ZN_FING 395 417 C2H2-TYPE.
 CC ZN_FING 423 445 C2H2-TYPE.
 CC ZN_FING 451 473 C2H2-TYPE.

FT ZN_FING 479 501 C2H2-TYPE.
 FT ZN_FING 529 529 C2H2-TYPE.
 FT ZN_FING 535 557 C2H2-TYPE.
 FT ZN_FING 563 585 C2H2-TYPE.
 FT ZN_FING 591 613 C2H2-TYPE.
 FT ZN_FING 617 639 C2H2-TYPE.
 FT ZN_FING 645 667 C2H2-TYPE.
 FT ZN_FING 673 695 C2H2-TYPE.
 SQ SEQUENCE 697 AA; 79552 MW; B574C89FFE55CEB4 CRC64;

Query Match 57.8%; Score 37; DB 1; Length 697;
 Best Local Similarity 80.0%; Pred. No. 48;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFOLKKNKK 10
 DB 515 CFSLSKLNK 524

RESULT 13
 TRFL_CAMDR
 ID TRFL_CAMDR STANDARD; PRT; 708 AA.
 AC Q9TUM0; Q9MZS5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactotransferrin precursor (lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 CX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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 CC EMBL; AJ131674; CAB53387.1; -;
 CC EMBL; AF165879; AAF82441.1; -;
 CC HSP; O77811; 1B1X.
 CC InterPro; IPR001156; Transferrin.
 CC Pfam; PF00405; transferrin; 2.
 CC PRINTS; PR00422; TRANSFERRIN.
 CC SMART; SM00094; TR_FER; 2.
 CC PROSITE; PS00205; TRANSFERRIN_1; 2.
 CC PROSITE; PS00206; TRANSFERRIN_2; 2.
 CC PROSITE; PS00207; TRANSFERRIN_3; 2.
 CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 CC Signal.
 CC SIGNAL 1 19 BY SIMILARITY.
 CC CHAIN 20 708 LACTOTRANSFERRIN.

```
T REPEAT 20 363 1.
T REPEAT 364 708 2.
T DISULFID 28 64 BY SIMILARITY.
T DISULFID 38 55 BY SIMILARITY.
T DISULFID 134 217 BY SIMILARITY.
T DISULFID 176 192 BY SIMILARITY.
T DISULFID 189 200 BY SIMILARITY.
T DISULFID 264 264 BY SIMILARITY.
T DISULFID 377 399 BY SIMILARITY.
T DISULFID 367 390 BY SIMILARITY.
T DISULFID 424 703 BY SIMILARITY.
T DISULFID 444 666 BY SIMILARITY.
T DISULFID 476 551 BY SIMILARITY.
T DISULFID 500 694 BY SIMILARITY.
T DISULFID 510 524 BY SIMILARITY.
T DISULFID 521 534 BY SIMILARITY.
T DISULFID 592 606 BY SIMILARITY.
T DISULFID 644 649 BY SIMILARITY.
T METAL 79 79 IRON 1 (BY SIMILARITY).
T METAL 111 111 IRON 1 (BY SIMILARITY).
T METAL 211 211 IRON 1 (BY SIMILARITY).
T METAL 272 272 IRON 1 (BY SIMILARITY).
T METAL 414 414 IRON 2 (BY SIMILARITY).
T METAL 452 452 IRON 2 (BY SIMILARITY).
T METAL 545 545 IRON 2 (BY SIMILARITY).
T METAL 614 614 IRON 2 (BY SIMILARITY).
T BINDING 140 140 ANION (BY SIMILARITY).
T BINDING 482 482 ANION (BY SIMILARITY).
T CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
T CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
T CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
T CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
T CONFLICT 261 261 F -> S (IN REF. 2).
T CONFLICT 304 304 G -> A (IN REF. 2).
T CONFLICT 330 330 S -> P (IN REF. 2).
T CONFLICT 492 494 LLS -> PLF (IN REF. 2).
T CONFLICT 506 506 L -> F (IN REF. 2).
T CONFLICT 609 609 A -> P (IN REF. 2).
T CONFLICT 642 642 R -> Q (IN REF. 2).
T SEQUENCE 708 AA; 77211 MW; 0B0C175A0B69D430 CRC64;
Query Match 57.8%; Score 37; DB 1; Length 708;
Best Local Similarity 58.3%; Pred. No. 49;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Y 1 CPOLKKNKKVR 12
b 38 CAQWQRKKVR 49
RESULT 14
AD5_HUMAN STANDARD; PRT; 784 AA.
P3151;
01-OCT-1993 (Rel. 27, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3 Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5)
(7B4 antigen) (CD144 antigen).
CDH5.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Endothelial cells;
MEDLINE=95353875; PubMed=7627717;
Breviario F.; Cavada L.; Corada M.; Martin-Padura I.; Navarro P.;
Golay J.; Introna M.; Gullino D.; Lampugnani M.G.; Dejana E.;
"Functional properties of human vascular endothelial cadherin
(7B4/cadherin-5), an endothelium-specific cadherin.";
Arterioscler. Thromb. Vasc. Biol. 15:1229-1239(1995).
```

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97362755; PubMed=9219219;
RA Ali J., Liao F., Martens E., Muller W.A.;
RT "Vascular endothelial cadherin (VE-cadherin): cloning and role in
RL endothelial cell-cell adhesion.";
RN [3]
RP Microcirculation 4:267-277(1997).
RX SEQUENCE FROM N.A.
RA PubMed=10861224;
RT Shimoyama Y., Tsujimoto G., Kitajima M., Natori M.;
RT "Identification of three human type-II classic cadherins and frequent
RT heterophilic interactions between different subclasses of type-II
RT classic cadherins.";
RL Biochem. J. 349:159-167(2000).
RN [4]
RP SEQUENCE OF 5-784 FROM N.A.
RX TISSUE=Brain;
RA PubMed=91283540; PubMed=2059658;
RT Suzuki S., Sano K., Tanihara H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins
RT in nervous tissue.";
RN [5]
RP Cell Regul. 2:261-270(1991).
RX PARTIAL SEQUENCE.
RA TISSUE=Endothelial cells;
RX MEDLINE=92394977; PubMed=1522121;
RA Lampugnani M.G., Resnati M., Raiteri M., Pigott R., Pisacane A.,
RA Houen G., Ruco L.P., Dejana E.;
RT "A novel endothelial-specific membrane protein is a marker of
RT cell-cell contacts.";
RL J. Cell Biol. 118:1511-1522(1992).
CC -!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
CC THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
CC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
CC SORTING OF HETEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A
CC IMPORTANT ROLE IN ENDOTHelial CELL BIOLOGY THROUGH CONTROL OF THE
CC COHESION AND ORGANIZATION OF THE INTERCELLULAR JUNCTIONS. IT
CC ASSOCIATES WITH ALPHA-CATENIN FORMING A LINK TO THE CYTOSKELETON.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. FOUND AT CELL-CELL
CC BOUNDARIES AND PROBABLY AT CELL-MATRIX BOUNDARIES.
CC -!- TISSUE SPECIFICITY: ENDOTHelial TISSUES AND BRAIN.
CC -!- SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD144 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd144.htm".
CC -----
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CC -----
CC EMBL; X79981; CAA56306.1; --
CC EMBL; U84722; AAB41796.1; --
CC EMBL; AB035304; BAA87418.1; --
CC EMBL; X59796; CAA42468.1; --
CC FIR; S24305; IJHUC5.
CC HSSP; F15116; INCUJ.
CC GlyscoSiteDB; P33151; --
CC Genew; HGNC:1764; CDH5.
CC MIM; 601120; --
CC InterPro; IPR002126; Cadherin.
CC InterPro; IPR000233; Cadherin_C_term.
CC Pfam; PF00028; cadherin; 5.
CC Pfam; PF01049; Cadherin_C_term; 1.
CC PRINTS; PR00205; CADHERIN.
CC SMART; SM00112; CA; 5.
CC PROSITE; PS00232; CADHERIN 1; 3.
CC PROSITE; PS0268; CADHERIN 2; 5.
CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
```

KW Signal. 1 25
FT SIGNAL 26 47
FT PROPEP 48 784
FT CHAIN 48 784
FT DOMAIN 48 784
FT TRANSMEM 594 620
FT DOMAIN 621 784
FT DOMAIN 48 151
FT DOMAIN 152 258
FT DOMAIN 259 372
FT DOMAIN 373 477
FT DOMAIN 478 593
FT DOMAIN 736 753
FT CARBOHYD 61 61
FT CARBOHYD 112 112
FT CARBOHYD 157 157
FT CARBOHYD 362 362
FT CARBOHYD 442 442
FT CARBOHYD 523 523
FT CARBOHYD 535 535
FT CONFLICT 517 517
SQ SEQUENCE 784 AA; 87516 MW; F643BFC222A599DE CRC64;

QY 3 QLKKNMKV 11
DB 86 QLKSLKKV 94
Search completed: February 21, 2003, 07:51:44
Job time : 7.2093 secs

Query Match 57.8%; Score 37; DB 1; Length 784;
Best Local Similarity 77.8%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FOLKKNMK 10
DB 379 FOLKENQK 387

RESULT 15
YEAS YEAST STANDARD; PRT; 282 AA.
AC P40003;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 31.4 kDa protein in GCN4-WEP1 intergenic region.
EN YELO05C.
CS Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
DX NCBI TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunkle-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren I., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; U18530; AAB64482.1;
DR SGD; S0000731; VAB2.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 31364 MW; 8F7CA122F91E491A CRC64;

Query Match 56.2%; Score 36; DB 1; Length 282;
Best Local Similarity 77.8%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.3
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M protein - protein search, using sw model

on: February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
(without alignments)
114.078 Million cell updates/sec

file: US-09-743-107b-96

effect score: 64

sequence: 1 CFQLKXNMKKV 12

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 671580 seqs, 206047115 residues

total number of hits satisfying chosen parameters: 671580

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase: SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertibrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	43	67.2	711	4	Q8TCD2
2	42	65.6	573	2	Q9S6F6
3	40	62.5	333	5	Q20562
4	39	60.9	38	4	Q3UCY5
5	39	60.9	222	10	Q9L265
6	39	60.9	282	16	Q97G23
7	39	60.9	339	10	Q9AW69
8	39	60.9	455	4	Q9BQK9
9	39	60.9	545	4	Q9H117
10	39	60.9	711	4	Q9H116
11	39	60.9	1162	5	Q9S011
12	39	60.9	1553	5	O77385
13	38.5	60.2	1167	10	Q94E36
14	38	59.4	325	10	Q9AYV6
15	38	59.4	2014	5	Q22774
16	37	57.8	108	11	Q9D5E5

17	37	57.8	125	4	Q9H960
18	37	57.8	253	5	Q9VZQ6
19	37	57.8	292	5	Q8SQS0
20	37	57.8	315	5	Q9SSH7
21	37	57.8	335	5	Q81888
22	37	57.8	357	13	Q919R0
23	37	57.8	425	4	Q9BSW9
24	37	57.8	546	16	Q98PL7
25	37	57.8	565	16	O8XJU2
26	37	57.8	718	5	Q23447
27	37	57.8	720	6	Q9N003
28	36	56.2	81	16	Q97PW0
29	36	56.2	104	16	Q97TB1
30	36	56.2	124	5	Q8T578
31	36	56.2	129	5	Q95Z48
32	36	56.2	129	5	Q8T4U9
33	36	56.2	136	5	O77176
34	36	56.2	167	10	Q9SR76
35	36	56.2	191	16	Q9JQR9
36	36	56.2	192	5	Q8WPY7
37	36	56.2	227	2	Q9X319
38	36	56.2	258	10	O80652
39	36	56.2	260	10	O80651
40	36	56.2	294	3	Q04005
41	36	56.2	295	10	O65376
42	36	56.2	315	16	O8Y311
43	36	56.2	320	2	Q937N3
44	36	56.2	512	13	Q9IAS1
45	36	56.2	538	13	Q9IAS0

ALIGNMENTS

RESULT 1

Q8TCD2 PRELIMINARY; PRT; 711 AA.
 AC Q8TCD2;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Lactotransferrin.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PROSTATE;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC02347; AAH22347.1;
 SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 67.2%; Score 43; DB 4; Length 711;

Best Local Similarity 63.6%; Pred. No. 27;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQLKXNMKKV 11
 ||| :|||
 Db 39 CFQWQNMKKV 49

RESULT 2

Q9S6F6 PRELIMINARY; PRT; 573 AA.
 ID Q9S6F6
 AC Q9S6F6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Urease (EC 3.5.1.5) (Urea amidohydrolase).
 GN UREC.
 OS Lactobacillus fermentum.

DC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 DC Lactobacillaceae; Lactobacillus.

DN NCBI_TaxID=1613;
 RN [1] :
 RP SEQUENCE FROM N.A.
 RC STRAIN=TK1214;
 RA Coton E., Visser J.J., Van Vuuren H.J.J.;
 RT "Urease operon of Lactobacillus fermentum";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DC -!- CATALYTIC ACTIVITY: UREA + H(2)O = CO(2) + 2 NH(3).
 CC -!- COFACTOR: EACH CHAIN BINDS TWO NICKEL IONS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE UREASE FAMILY.
 CC EMBL; AF120718; AAD22480.1; -.
 DR HSSP; P41020; 1UBP.
 DR InterPro; IPR001924; UreaseA.
 DR Pfam; PF00449; urease; 1.
 DR PROSITE; PS01120; UREASE_1; 1.
 DR PROSITE; PS01145; UREASE_2; 1.
 KW Hydrolase; Metal-binding; Nickel.
 SQ SEQUENCE 573 AA; 61823 MW; 4D325C6C4A21559C CRC64;

Query Match 65.7%; Score 42; DB 2; Length 573;
 Best Local Similarity 66.7%; Pred. No. 34;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

2Y 1 CFQLKKNKKVR 12
 [1] :
 DB 379 CWQLASKMKKVR 390
 [1] :
 [1] :
 [1] :

RESULT 3

220562
 ID Q20562 PRELIMINARY; PRT; 333 AA.
 AC Q20562;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 38.1 kDa protein.
 EN F48D6.2.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 CC NCBI_TaxID=6239;
 RN [1] :
 RP SEQUENCE FROM N.A.
 RC STRAIN=ERISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ERISTOL N2;
 RA Geisel C., Bradshaw H.;
 RT "The sequence of C. elegans cosmid F48D6.";
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ERISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U58732; AB00596.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 333 AA; 38150 MW; B2A5ED557CDBA5C9 CRC64;

Query Match 62.5%; Score 40; DB 5; Length 333;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

2Y 1 CFQLKKNKKVR 12

Db 198 CFLRKWKVK 209
 [1] :
 [1] :
 [1] :

RESULT 4

Q9UCY5
 ID Q9UCY5 PRELIMINARY; PRT; 38 AA.
 AC Q9UCY5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Lactoferrin homolog (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96081613; PubMed=8551695;
 RA Sato I.;
 RT "Characterization of the 84-kDa protein with ABH activity in human
 RT seminal plasma.";
 RL Jpn. J. Legal Med. 49:281-293(1995).
 DR HSSP; P02788; IBKA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 SQ SEQUENCE 38 AA; 4459 MW; 0402F4905EBDBB CRC64;

Query Match 60.9%; Score 39; DB 4; Length 38;
 Best Local Similarity 63.6%; Pred. No. 11;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 POLKKNKKVR 12
 [1] :
 [1] :
 [1] :

Db 21 FQWQNNKKVR 31
 [1] :
 [1] :
 [1] :

RESULT 5

Q9LZ65
 ID Q9LZ65 PRELIMINARY; PRT; 222 AA.
 AC Q9LZ65;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Rna binding protein-like (AT5G04600/T32M21_200) (Putative RNA binding
 DE protein)
 GN T32M21_200 OR AT5G04600.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terry N., Ardiles W., Buyschaert C., Dasseville R.,
 RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
 RA Villarroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,
 RA Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;

"Arabidopsis ORF clones."; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

[4] SEQUENCE FROM N.A.

Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

[5] SEQUENCE FROM N.A.

Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full length cDNA of gene At5g04600 (GI:15238220)."; Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

EMBL; AL162875; CAB85566.1; -

EMBL; AY055787; AAL06954.1; -

EMBL; AF378899; AAK55702.1; -

EMBL; AY063822; AAL36178.1; -

InterPro: IPR000504; RNA_rec_mot.

Pfam: PF00076; rrm; 1.

SMART; SM00360; RRM; 1.

PROSITE; PS0102; RRM; 1.

SEQUENCE 222 AA; 25262 MW; BA47EAE8D8B2F153 CRC64;

Query Match 60.9%; Score 39; DB 10; Length 222;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LKONMKV 11

|||||

9 LKONMKV 16

SULT 6

7G23

Q97G23 PRELIMINARY; PRT; 282 AA.

Q97G23; 01-OCT-2001 (TrEMBLrel. 18, Created)

01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

01-OCT-2001 (TrEMBLrel. 18, Last annotation update)

Unclassified conserved protein.

CAC2549.

Clostridium acetobutylicum.

Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

NCBI_TaxID=1468;

[1]

SEQUENCE FROM N.A.

STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE=21359325; PubMed=11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tarusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum."; J. Bacteriol. 183:4823-4838(2001).

EMBL; AE007753; AAK80500.1; -

Complete proteome.

SEQUENCE 282 AA; 31629 MW; E94EE94D502A5730 CRC64;

Query Match 60.9%; Score 39; DB 16; Length 282;

Best Local Similarity 58.3%; Pred. No. 60;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFOLKKNMKV 12

DB 241 CQOLKENISKLR 252

RESULT 7

Q9AW69 PRELIMINARY; PRT; 339 AA.

ID Q9AW69

AC Q9AW69

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hypothetical 41.4 kDa protein.

OS Guillardia theta (Cryptomonas phi).

OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.

OX NCBI_TaxID=55529;

[1]

RN SEQUENCE FROM N.A.

RX MEDLINE=20087226; PubMed=10618395;

RA Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M., Cavalier-Smith T., Maier U., Douglas S.; "Chloroplast protein and centrosomal genes, a tRNA intron, and odd telomeres in an unusually compact eukaryotic genome, the cryptomonad nucleomorph."; Proc. Natl. Acad. Sci. U.S.A. 97:200-205(2000).

[2]

RN SEQUENCE FROM N.A.

RX MEDLINE=2123349; PubMed=11323671;

RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L., Wu X., Reith M., Cavalier-Smith T., Maier U.; "The highly reduced genome of an enslaved algal nucleus."; Nature 410:1091-1096(2001).

RL Nature 410:1091-1096(2001).

DR EMBL; AJ010592; CAC27001.1; -

KW Hypothetical protein.

SQ SEQUENCE 339 AA; 41403 MW; B24EE99E30715629 CRC64;

Query Match 60.9%; Score 39; DB 10; Length 339;

Best Local Similarity 80.0%; Pred. No. 70;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FOLKKNMKV 11

|||||

DB 179 FNLKONKKV 188

RESULT 8

Q9BQK9 PRELIMINARY; PRT; 455 AA.

ID Q9BQK9

AC Q9BQK9

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE DU322G13.2:2 (zinc finger protein FLJ21794, isoform 2).

GN DU322G13.2.

[1]

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

RN SEQUENCE FROM N.A.

RA Lovell J.; Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AL096677; CAC34610.1; -

DR HSSP; Q05516; 1CS3.

DR InterPro: IPR000210; BTB_POZ.

DR InterPro: IPR000822; Znf_C2H2.

DR Pfam; PF00851; BTB; 1.

DR Pfam; PF00096; zf-C2H2; 5.

DR SMART; SM00225; BTB; 1.

DR SMART; SM00355; Znf_C2H2; 5.

```

R PROSITE; PS00097; BTB; 1.
R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
R PROSITE; PS00157; ZINC_FINGER_C2H2_2; 5.
W DNA-binding; Metal-binding; Zinc-finger.
Q SEQUENCE 455 AA; 51357 MW; 33099B1B7F7CB757 CRC64;

Query Match
Best Local Similarity 60.9%; Score 39; DB 4; Length 455;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQKKKQM 8
  |||||
b 125 CFQKKKQM 132

RESULT 9
9H117 QSH117 PRELIMINARY; PRT; 545 AA.
C QSH117;
T 01-MAR-2001 (TRENBLrel. 16, Created)
T 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
T 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
E DJ322G13.2.1 (zinc finger protein FLJ21794, isoform 1).
N DJ322G13.2.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
P Lovell J.;
A Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
L Submitter; (MAR-2001) to the EMBL/GenBank/DBJ databases.
R HSSP; P07248; 1ARF.
R InterPro; IPR000210; BTB_POZ.
R InterPro; IPR000822; Znf_C2H2.
R Pfam; PF00651; BTB; 1.
R Pfam; PF00096; zf-C2H2; 8.
R ProDom; PD000003; Znf_C2H2; 1.
R SMART; SM00225; BTB; 1.
R SMART; SM00355; Znf_C2H2; 8.
R PROSITE; PS00097; BTB; 1.
R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
R PROSITE; PS00157; ZINC_FINGER_C2H2_2; 8.
W DNA-binding; Metal-binding; Zinc-finger.
Q SEQUENCE 545 AA; 61982 MW; AA9820E319C361E CRC64;

Query Match
Best Local Similarity 60.9%; Score 39; DB 4; Length 545;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CFQKKKQM 8
  |||||
b 125 CFQKKKQM 132

RESULT 10
9H116 QSH116 PRELIMINARY; PRT; 711 AA.
C QSH116;
T 01-MAR-2001 (TRENBLrel. 16, Created)
T 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
T 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
E DJ322G13.2.3 (zinc finger protein FLJ21794, isoform 3).
N DJ322G13.2.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
P Lovell J.;
A Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
L Submitter; (MAR-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AL096677; CAC03438.2; -.
DR HSSP; P08047; 1SP2.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR000822; Znf_C2H2.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00096; zf-C2H2; 10.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00355; Znf_C2H2; 10.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 9.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 10.
KW DNA-binding; Metal-binding; Zinc-finger.
SQ SEQUENCE 711 AA; 80491 MW; 9209B850193BCF1A CRC64;

Query Match
Best Local Similarity 60.9%; Score 39; DB 4; Length 711;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFQKKKQM 8
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Db 125 CFQKKKQM 132

RESULT 11
Q95011 PRELIMINARY; PRT; 1162 AA.
ID Q95011;
AC Q95011;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE F2966.1 protein.
GN F2966.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1];
RP SEQUENCE FROM N.A.
RA Harris B.R.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2];
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
  investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z78543; CAB01753.1; -.
DR HSSP; P01003; 3OVO.
DR InterPro; IPR002350; kazal.
DR InterPro; IPR001239; Kazal_inhib.
DR Pfam; PF00050; kazal; 14.
DR PRINTS; PRO0290; KAZALINHTR.
DR SMART; SM00280; KAZAL; 15.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
KW Serine protease inhibitor.
SQ SEQUENCE 1162 AA; 130179 MW; 080AEFC277E28CE8 CRC64;

Query Match
Best Local Similarity 60.9%; Score 39; DB 5; Length 1162;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFQKKKMKVR 12
  |||||
Db 943 CFQKKKMKVTIQ 954

RESULT 12
O77385 PRELIMINARY; PRT; 1553 AA.
ID O77385
AC O77385;
DT 01-NOV-1998 (TRENBLrel. 08, Created)

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1 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
2 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
3 CDC2-related protein kinase
4 PFC0755C, MAU3P6.10.
5 Plasmodium falciparum (isolate 3D7).
6 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
7 NCBI_TaxID=36329;
8 [1]
9 SEQUENCE FROM N.A.
10 STRAIN=3D7;
11 MEDLINE=99376085; PubMed=10448855;
12 Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
13 Churcher C.M., Craig A., Davies R.M., Devlin K., Feltham T.,
14 Gentles S., Gilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
15 Horrocks P., Jagals K., Jaseal B., Kyes S., McLean J., Moule S.,
16 Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
17 Rutter S., Skelton J., Squares S., Squares S., Sulston J.E.,
18 Whitehead S., Woodward J.R., Newbold C., Barrett B.G.;
19 "The complete nucleotide sequence of chromosome 3 of Plasmodium
20 falciparum.";
21 Nature 400:532-538(1999).
22 -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
23 EMBL; Z98551; CAB1141.1;
24 InterPro; IPR000719; Euk_PKinase.
25 InterPro; IPR002290; Ser_thr_pkinase.
26 Pfam; PF00069; pkinase; 1.
27 ProDom; PD000001; Euk_PKinase; 2.
28 PROSITE; PS0107; PROTEIN KINASE ATP; 1.
29 PROSITE; PS0011; PROTEIN KINASE DOM; 1.
30 PROSITE; PS00108; PROTEIN KINASE ST; 1.
31 ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
32 SEQUENCE 1553 AA; 182218 MW; E23D3C3416F1E8EF CRC64;
33
34 Query Match 60.9%; Score 39; DB 5; Length 1553;
35 Best Local Similarity 77.8%; Pred. No. 2.5e+02;
36 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
37
38 4 LKONKMKV 12
39 :|||||:
40 39 MKONKMKV 47
41
42 SULT 13
43 4E36
44 Q94E36 PRELIMINARY; PRT; 1167 AA.
45 Q94E36;
46 01-DEC-2001 (TrEMBLrel. 19, Created)
47 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
48 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
49 OSJNB0032H9.19 protein.
50 Oryza sativa (Rice).
51 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
52 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
53 Ehrhartoideae; Oryzoideae; Oryza.
54 NCBI_TaxID=4530;
55 [1]
56 SEQUENCE FROM N.A.
57 STRAIN=CV. NIPPONBARE;
58 Sasaki T., Matsumoto T., Yamamoto K.;
59 "Oryza sativa nipponbare (CA3) genomic DNA, chromosome 1, BAC
60 clone:OSJNB0032H9.19.";
61 Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
62 EMBL; AP003219; BAB61186.1;
63 InterPro; IPR003653; SUMO protease.
64 Pfam; PF02902; Peptidase C48; 1.
65 SEQUENCE 1167 AA; 131408 MW; 6308AB28A292C1F9 CRC64;
66
67 Query Match 60.2%; Score 38.5; DB 10; Length 1167;
68 Best Local Similarity 72.7%; Pred. No. 2.4e+02;
69 Matches 8; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
70
71 1 CFQLKKNMKV 11
72 :|||||:
73
74 Db 1043 CFQLKKNMKV 1052
75
76 RESULT 14
77 Q9AVY6 PRELIMINARY; PRT; 325 AA.
78 AC Q9AVY6;
79 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
80 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
81 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
82 DE Hypothetical 39.4 kDa protein.
83 OX Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
84 NCBI_TaxID=55529;
85 [1]
86 SEQUENCE FROM N.A.
87 MEDLINE=20087226; PubMed=10618395;
88 RA Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M.,
89 Cavalier-Smith T., Maier U., Douglas S.;
90 "Chloroplast protein and centosomal genes, a tRNA intron, and odd
91 telomeres in an unusually compact eukaryotic genome, the cryptomonad
92 nucleomorph.";
93 Proc. Natl. Acad. Sci. U.S.A. 97:200-205(2000).
94 [2]
95 SEQUENCE FROM N.A.
96 MEDLINE=2123349; PubMed=11323671;
97 RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.,
98 Wu X., Reith M., Cavalier-Smith T., Maier U.;
99 "The highly reduced genome of an enslaved algal nucleus.";
100 Nature 410:1091-1096(2001).
101 RL EMBL; AJ010592; CAC27085.1;
102 DR EMBL; AJ010592; CAC27085.1;
103 KW Hypothetical protein.
104 SEQUENCE 325 AA; 39399 MW; 27D35E07CD82F083 CRC64;
105
106 Query Match 59.4%; Score 38; DB 10; Length 325;
107 Best Local Similarity 54.5%; Pred. No. 1e+02;
108 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
109
110 QY 1 CFQLKKNMKV 11
111 :|||||:
112 Db 130 CVLKKNKIKI 140
113
114 RESULT 15
115 Q22774 PRELIMINARY; PRT; 2014 AA.
116 AC Q22774; O01703; O01984;
117 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
118 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
119 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
120 DE Hypothetical 221.3 kDa protein T25C12.3 in chromosome X.
121 T25C12.3.
122 OS Caenorhabditis elegans.
123 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
124 Rhabditidae; Peloderinae; Caenorhabditis.
125 NCBI_TaxID=6239;
126 [1]
127 SEQUENCE FROM N.A.
128 STRAIN=BRISTOL N2;
129 Kershaw J.;
130 Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
131 -!- SIMILARITY: WEAK, TO C.ELEGANS ZK1193.2 AND TO THE C-TERMINAL OF
132 COLLAGENS.
133 EMBL; Z66566; CAA91487.1;
134 EMBL; Z78543; CAA91487.1; JOINED.
135 EMBL; Z93779; CAA91487.1; JOINED.
136 EMBL; Z93779; CAB07849.1;
137 EMBL; Z78543; CAB07849.1; JOINED.
138 EMBL; Z66566; CAB07849.1; JOINED.
139 EMBL; Z78543; CAB01757.1;
140 EMBL; Z93779; CAB01757.1; JOINED.
141 EMBL; Z66566; CAB01757.1; JOINED.
142 WormPep; T25C12.3; CE18966.

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>R InterPro; IPR000561; EGF-like.
>R InterPro; IPR01304; Lectin_C.
>R InterPro; IPR02035; VWFA_A.
>R Pfam; PF00059; lectin_C; 1.
>R SMART; SM0034; CLECT; 1.
>R SMART; SM0181; EGF; 3.
>R SMART; SM0327; VWA; 1.
>R PROSITE; PS0041; C TYPE LECTIN_2; 1.
>R PROSITE; PS0022; EGF_1; UNKNOWN_5.
>R PROSITE; PS01186; EGF_2; 3.
>R PROSITE; PS0234; VWFA; 1.
>W Hypothetical protein.
>Q SEQUENCE 2014 AA; 221261 MW; 65E3BC76440C73BB CRC64;

Query Match      59.4%; Score 38; DB 5; Length 2014;
Best Local Similarity 87.5%; Pred. No. 4.7e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

>Y 2 FOLKKNMK 9
>b 1410 FOLKKNLK 1417

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Search completed: February 21, 2003, 08:00:50
 Job time : 23.6744 secs